Mycoplasma galiise M.gallisepticum 66 Mycobacterium gall PMGA 1.2 protein o Amino acid sequenc MG-4 antigan. AA Amino acid sequenc MG-3 antigen. AA

MG-3 antigen. AA Staphylococcus aur Staphylococcus aur

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Perfect score: Sequence: Scoring table:

Sarched:

Database

OM protein

Run on

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Chimeric; Marek's disease virus; outer membrane protein; fusion protein; antigen; vaccine; poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.64
/note= "derived from Marek's disease virus gB protein"
65.456
/note= "derived from M. gallisepticum antigenic protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid Marek's disease virus/M. gallisepticum 40 K-S protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Marek's disease gammaherpesvirus.
Chimeric - Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                 AAYS8435
AAB69508
AAW89801
AAU34339
                                                                                                                                                                                                                                                       AAW55640
AAY17187
           AAR63226
AAR79910
AAW11978
                                                                                                AAU37403
AAG83030
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AAU34389
AAU37490
                                                                                                                                                                                                                       AAR95273
AAU34320
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AAU34412
AAU37520
                                           AAR56973
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                                                                 AAR06439
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                                                                                                                                                                                                                                              AAU37374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW36050 standard; Protein; 456 AA
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 97WO-JP01084
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28-MAR-1997;
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Hybrid Marek's dis
Mycoplasma gallise
Mycoplasma gallise
Mycoplasma gallise
Mycoplasma gallise
Amino acid sequenc
MG-1 antigen. AA
TMG-1 antigen. AA
M.gallisepticum 26
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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1984.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*
110: /SIDSI/gcgdata/hold-geneseqy-embl/AA1980.DAT:*
121: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1980.DAT:*
122: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1991.DAT:*
133: /SIDSI/gcgdata/hold-geneseqy-geneseqp-embl/AA1992.DAT:*
143: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
144: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
155: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1992.DAT:*
165: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
176: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
177: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
188: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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180: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
180: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
215: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
216: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
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218: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
218: /SIDSI/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                     (without alignments)
783.980 Million cell updates/sec
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                                                                                                                                         CMSITKKDANPNNGQTQLEA.....SSNENNADKIPGYRRPGTFL
                                                                       June 12, 2002, 10:42:12 ; Search time 55.68 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAR63230
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Gapop 10.0 , Gapext 0.5
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57.2
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1998 1994 1910 1856 1612 1612 1162 1142 1142

Score

Result No.

Staphylococcus aur Partial PMGA 1.3 p Mycobacterium gall Staphylococcus aur Staphylococcus aur

Staphylococcus Staphylococcus

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Yanagida

Tsuzaki Y,

97WO-JP01084 96JP-0103548

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Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                               Disclosure; Page 22-30; 51pp; Japanese.
                                                                                                                                         (JAPG ) NIPPON ZEON KK
                                                                                                                                                                                                     WPI; 1997-503046/46
                                                                                                                                                                                                                     N-PSDB; AAT96596
                                                                           28-MAR-1997;
                                                                                                          29-MAR-1996;
                WO9736924-A1
                                              09-0CT-1997
                                                                                                                                                                       Saito S,
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                                                                                                                                      This sequence represents the chimeric protein 40 K-S which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric; Marek's disease virus; outer membrane protein; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..672 "derived from Marek's disease virus gB protein" 693..1086
                                                                                                                                                                                                                                                                                                                                                                        64 cmsitkkdanpnnggtgleaarmeltdlinakamtlasigdyakleasissayseaetvn 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein comprising herpes virus outer membrane protein and nic polypeptide – for prevention of infection by Mycoplasma
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                                                                                                                                                                                                                                                                                                 DB 18; Length 456;
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                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 1998; DB 18; Best Local Similarity 100.0%; Pred. No. 2.1e-126; Matches 393; Conservative 0; Mismatches 0;

    Marek's disease gammaherpesvirus.
    Mycoplasma gallisepticum.

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                                                                                                        Disclosure; Page 16-19; 51pp; Japanese
                                                                           gallisepticum, especially in poultry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen; vaccine; poultry
                                                              polypeptide
WPI; 1997-503046/46.
N-PSDB; AAT96595.
                                                                                                                                                                                                                                                   456 AA;
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Chimeric
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Region
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This sequence represents the chimeric protein 40 K-C which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 360
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                                                                                                                                                                                           Length 1086;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                         99.8%; Score 1994; DB 18; 99.7%; Pred. No. 1.2e-125; live 0; Mismatches 1;
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                                                                                                                                                                                           Query Match 99.8
Best Local Similarity 99.7
Matches 392; Conservative
                                                                                                                                     1086 AA;
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387 mnkvapmigniylssnennadki 409
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30-SEP-1993;
                                                                                                  23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                                                A restriction fragment of the insert of M.gallisepticum genomic clone pUM-67 containing an open reading frame was sequenced (AAQ77857). The ORF encodes an antiquente polypeptide (AAR63230). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNYGLQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide -
the production
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                                                                           1..615
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 615;
                     recombinant avipox virus; live vaccine; mycoplasma antigen.
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                                                                                                                                                                                                                                                                                                                 encoding a
useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1910; DB 15;
Pred. No. 2.5e-120;
                                                                                                                                                                                                                                                Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
Mycoplasma gallisepticum antigen (UM-67)
                                                                                                                                                                                                                                                                                                                 Recombinant avipox virus combining DNA exhibiting antigenicity of mycoplasma,
                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 87-91; 123pp; Japanese.
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                         Funato H, Irica...
Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.6%;
                                                                                                                                                       94WO-JP00541
                                                                                                                                                                                        93JP-0245625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0074139
                                                                                                                                                                                                             (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                           gallisepticum
                                                                                                                                                                                                                                                                               WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                                          Saitos,
                                                                                                                                                                                                                                                                                                                                       of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 AA;
                                                                                                                                                                                                                                                                                           N-PSDB; AAQ77857.
                                                                                                                                                      31-MAR-1994;
                                                                                                                                                                            31-MAR-1993;
30-SEP-1993;
                                                                                                            WO9423019-A
                                                                                                                                13-OCT-1994
                                            Mycoplasma
                                                                                                                                                                                                                                                s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                          Saeki S,
                                                                           Protein
                                                                                                                                                                                                                                                 Aoyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
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A restriction fragment of the insert of M.gallisepticum genomic clone pUM-66 containing an open reading frame was sequenced (AAQ77856). The ORF encodes an antigenic polypeptide (AAR63229), A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CMSITKKDANPNNGGTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nnlnatleglkmaktnlesaingantdkttfdnehpnlveaykalkttlegratnlegls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide -
the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                 codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 610;
                                                                                                                                                           recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                     Location/Qualifiers
1..610
/note= "Trp residues correspond to TGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant avipox virus combining DNA encoding a exhibiting antigenicity of mycoplasma, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1856; DB 15;
Pred. No. 1.1e-116;
); Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                     Mycoplasma gallisepticum antigen (UM-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 78-81; 123pp; Japanese.
  A
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aitos, Takahashi K;
  610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.98;
AAR63229 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                  94WO-JP00541.
                                                                                                                                                                                                                                                                                                                                                                                                                                          93JP-0074139.
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(SHIO ) SHIONOGI & CO LTD.
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-333181/41.
N-PSDB; AAQ77856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a live vaccine
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361 387 AAR44493;

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AAR44493

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The plasmid pUTTW-IP contains a sequence (the TTW-I gene) coding for the 40KD antigen of Mycoplasma gallisepticum under the control of a synthetic promoter. A 1300 bp restriction fragment containing the promoter-ORF sequence was excised and was used in the construction of plasmid pNZ7929-R2. This in turn was involved in the construction of a recombinant avipox virus vector comprising the TTW-I gene, DNA encoding the signal membrane anchor peptide from Newcastle Disease Virus haemagglutinin neuraminidase and FPV sequences. The recombinant avipox virus is useful as a live vaccine
                                                                                                                                                 nnlnatleqlkmaktnlesainqantdkttfdnehpnlveaykalkttleqratnlegla 146
                         PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                           recombinant avipox virus; live vaccine; mycoplasma 40kD antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "corresponds to a NNN codon'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "corresponds to a NNN codon"
                                                                                                                                                                                                       301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 71-74; 123pp; Japanese.
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Misc-difference 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funato H, Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi K;
                                                                                                                                                                                                                                                                                  AAR63227 standard; Protein; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0074139.
93JP-0245625.
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                                                                                                                                                                                                                                                                                                                                         23-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ77854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1993;
30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9423019-A
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                                                                                                                                                                                                                                                                                                              AAR63227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aoyama
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                                 121
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                                                                                                                                                                                                                                                            RESULT
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence coding for the 40kDa antigen was obtained by PCR amplification of M.gallisepticum genomic DNA. The antigen reacts with Mycoplasma-immune or Mycoplasma-infected serum and can be used as a vaccine to protect fowl from M.gallisepticum infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 368;
                                                                                                                                                                                                                                                                                                                                                                                              /note= "corresponds to NNN codon in AAQ53419"
283
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum antigen and DNA coding for it for vaccination of fowl against mycoplasma infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1612; DB 14;
Pred. No. 1.4e-100;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ś
                                                                                                                                                                                                                                                                                                                                Vaccine; mycoplasma infection; poultry; fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohkawa
                                                                                                                                                                                                                                                                                                    Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 23-26; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aoyama S, Fujisawa A, Iritani Y,
                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                        AAR44493 standard; Protein; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                          MNKVAPMIGNIYLSSNENNADK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.7%;
illarity 95.0%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93WO-JP00715
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ53419
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1993;
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nes 320;
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Sequence

Query Match

Best Loca Matches

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Gaps 9 86

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180 206 240 300

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AAQ94711 encodes AAR76955 Mycoplasma gallisepticum antigenic protein TTM-1. TTM-1 can be used as a vaccine for M. gallisepticum infectious diseases in poultry, and as a diagnostic agent for
                                                                                                                                                                                                                1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                  241 PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Mycoplasma gallisepticum (MG1) polypeptide.
                                                                                                                                                                                                       STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                                                                                                                              ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This amino acid sequence of MG1 is encoded by M1 DNA and elicits
                                                                                 Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iritani Y,
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Mycoplasma gallisepticum
                                                                               80.3%; Score 1604; DB 16;
llarity 94.4%; Pred. No. 4.7e-100;
Conservative 7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                            301 YKLNNGNVOQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum; Poultry vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Каподама
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NIPPON ZEON KK.
) SHIONOGI SEIYAKU KABUSHIKI KAISHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig.la; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                  AAP93646 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89EP-0005441
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma gallisepticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-358393/49.
                                                                                Query Match
Best Local Similarity
Matches 318; Conserv
                                                  368 AA;
                             M. gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN92568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kodama K,
                                                                                                                                                                                                                                                                                                                                                                                                                      AAP93646;
                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JAPG
(SHIO
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AAP93646
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                                                                                                                                NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                   ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
                                                                                                                                                                                                                          PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 300
                                                                                                                                                                                                                                                                Gaps
                                                                                       A new antigenic protein which reacts with Mycoplasma gallisepticum is useful in a component vaccine for use against poultry infected with M. gallisepticum.
                                                                     ;
0
                                                  Length 368;
to protect against infection by Mycoplasma gallisepticum.
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigenic protein; vaccine; poultry; diagnosis; TTM-1.
                                               Score 1612; DB 15;
Pred. No. 1.4e-100;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum antigenic protein TTM-1
                                                                                                                                                                                                                                                                                                       YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note- "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  AAR76955 standard; Protein; 368
                                                 80.7%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0213102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum.
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHIO ) SHIONOGI & CO
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N-PSDB; AAQ94711.
                                                           Similarity
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                    368
                                                Query Match
Best Local Simi.
Matches 320;
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                     Sequence
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CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-169109/22.
                                                                                                                                                                                                            AAR05082 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ04687
                                                                                                                                                                                                                                                                          TMG-1 antigen.
                                                                                                                                                                                                                                                                                                                    JP02111795-A.
                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1989;
                                                                                                                                                                                                                                                       08-OCT-1990
                                                                                                                                                                                                                                                                                                                                                            02-JUN-1989;
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antigen-antibody reaction with anti-MG poultry sera. It can be used as a vaccine to prevent and diagnose MG infection. Doseage is at least 1 micro gram vaccine / kg. No acute toxicity was noted with a dose of 5 mg / kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal bacterial enzyme sequence.

See also AAR05081-2 and AAR06437-41.
                                                                                                                                                                                                              61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                   121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                            1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                            181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235
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                                                                       235;
                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.2%; Score 1142; DB 11; Best Local Similarity 97.0%; Pred. No. 2.9e-69; Matches 228; Conservative 3; Mismatches 4;
                                                                      Score 1142; DB 10;
Pred. No. 2.9e-69;
                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum; poultry; vaccine.
                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig la; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                    235
                                                                       57.2%;
97.0%;
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                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                           Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-169109/22.
N-PSDB; AAQ04686.
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                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                MG-1 antigen
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DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera." It may also be ligated to other DNA to produce fusion proteins with an N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                   NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                    STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 cmsitkkdanpnngqtqlqaarmeltdlinakartlaslqdyakieaslssayseaetvn 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
Diagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.2%; Score 1142; DB 11; Length 261; 97.0%; Pred. No. 3.4e-69; 1ve 3; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum; poultry; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89JP-0136343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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This AA sequence of TMG-1 is encoded by TM-1 base sequence. It has the same sequence as that of a polypeptide expressed in Mycoplasma gallisepticum in nature. When the corresponding DNA sequence is inserted 'into a recombinant vector used to transform a host the antigen protein produced can be used as a vaccine to prevent and diagnose MG infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE-QKT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 NADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JAPG ) NIPPON ZEON KK; (SHIO) SHIONOGI SEIYAKU KABUSHIKI KAISHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antigenic proteins of Mycoplasma gallisepticum - useful as
                 181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanagida N, Kamogawa K, Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid (AA) sequence of TMG-1 polypeptide.
                                                                                                                                                                                                                                                            Mycoplasma gallisepticum; Poultry vaccine; ss;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig.2; 31pp; English.
                                                                                                                     AAP93959 standard; protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.9%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                89EP-0005441.
                                                                                                                                                                                                                                                                                                                                                                                                                                88JP-0136343.
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.9
Best Local Similarity 96.2
Matches 227; Conservative
                                                                                                                                                                                                                                                                                              Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1989-358393/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN92574
                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kodama K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of a 261 amino acid protein encoded by a fragment of the Mycoplasma gallisepticum genome. The encoding sequence and the sequence of AAT04075 (encoding a 661 amino acid protein) can be used to detect M.gallisepticum using probes based on nucleotides 1125-1648 and primers based on nucleotides 449-466, the complement of bases 893-919, 1908-1934 and the complement of bases 2184-2210 of AAT04075 and a probe based on nucleotides 718-41 of the DNA encoding this protein. The method using these sequences is faster i.e. is able to detect M.gallisepticum, which causes avian chronic respiratory diseases, within one day, from avian secretions, washings from the lung, respiratory tract, nasal cavity, etc.
NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
                                                                   Detection of Mycoplasma gallisepticum - for the quick detection, i.e. within one day, of avian chronic respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1142;
                                                                                                                                                                                                                                                                          M.gallisepticum 261 amino acid protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 10-11; 11pp; Japanese.
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                                                                                                                                                                   AAR79911 standard; Protein; 261
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97.0%;
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                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                              Mycoplasma gallisepticum.
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N-PSDB; AAT04076.
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                                                                                                                                                                                                                                                                                                                                                                                            JP07236498-A.
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                                                                                                                                                                                                                                         19-JUL-1996
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Matches 228;
                                                                                                                                                                                                       AAR79911;
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Length 261;

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Matches 185; Conservative
                                                            380 ----ADKIPGY 386
                                                                                ptavtvdllkgy 467
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N-PSDB; AAT04075.
                                                                                                                                                                                                                                                                           Misc-difference 220
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                                                                                                                                                                                                                                                                                                                                                                    JP07236498-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                     A restriction fragment of the insert of M.gallisepticum genomic clone pUM-81 containing an open reading frame was sequenced (AAQ77853). The ORF encodes an antigenic polypeptide (AAR63226). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NNINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 180
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                                                                                                                                                                                                                                                                                                                    recombinant avipox virus combining DNA encoding a polypeptide -exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                            1..661
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.3%; Score 806; DB 15; Length 661;
42.8%; Pred. No. 4.4e-46;
iive 62; Mismatches 123; Indels 65
                                                           recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                 Ohsawa I;
                                                                                                                                                                                                                                                                 Ohkawa S,
                                        Mycoplasma gallisepticum antigen (UM-81).
                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 61-65; 123pp; Japanese.
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                 Iritani Y,
                                                                                                                                                                                                                                                                        Saitos, Takahashi K;
                                                                                                                                                                                  94WO-JP00541.
                                                                                                                                                                                                               93JP-0245625.
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                    (first entry)
                                                                                                                                                                                                                                             SHIO ) SHIONOGI & CO LTD.
                                                                                Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                   JAPG ) NIPPON ZEON KK.
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                                                                                                                                                                                                                                                                                             WPI; 1994-333181/41.
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Best Local Similarity
Matches 185; Conserv
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                                                                                                                                                                                                               30-SEP-1993;
                    23-JUN-1995
                                                                                                                                           WO9423019-A.
                                                                                                                                                               13-OCT-1994
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AAR63226;
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                                                                                                             Protein
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            avian chronic respiratory disease; respiratory tract; nasal cavity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection; probe; primer; PCR; amplification; secretion; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 661;
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42.8%; Pred. No. 4.4e-46;
tive 62; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.gallisepticum 661 amino acid protein.
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multivalent live vaccines, also new probes for detecting Mycoplasma
and manipulating its genome
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Best Local Simi
Matches 169;
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                                                                                                                    -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 293
                                                                                                                                                     ANNVGLQYKLNNGNVQQVEF-----ATSTSAN--NTTANP-----TPAVDEIKVAKIV 339
                                                                                                                                                                                         340 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS-------NENN 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New promoter region from a Mycoplasma gallisepticum adhesin gene useful when coupled to foreign antigen gene, for prodn. of
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/label- Sig_peptide
/note- "the signal peptide shows homology to
the pMGAl.3 signal peptide"
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93AU-0050593.
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N-PSDB; AAT51531.
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10-NOV-1993;
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                                                                                                                        Adhesin pWGA1.2 (AAW11978) and adhesin pWGA1.3 fragment (AAW11979) are products of gene sequences (see also AAF15191) isolated from Mycoplasma gallisepticum. DAA constructs incorporating the promoter and/or signal sequences of the pWGA genes can be used in the produ. of multivalent live vaccines. The signal peptide sequence is utilised where attachment of an exogenous antigen gene to the mycoplasma cell membrane is required.
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Similarity 41.1%; Pred. No. 7.7e-40;
59; Conservative 60; Mismatches 124;
Disclosure; Fig 3; 81pp; English.
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4.5	Compugen Ltd.	,
enCore version 4.5	- 2000	
GenCore	(c) 1993 - 2000 (
	Copyright (

OM protein - protein search, using sw model

June 12, 2002, 10:46:22 ; Search time 29.99 Seconds (without alignments) 1259.190 Million cell updates/sec Run on:

US-09-147-052-2_COPY_64_456 1998 1 CMSITKKDANPNNGQTQLEA......SSNENNADKIPGYRRPGTFL 393 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	or surface prot	surface	surface	surface	glutinin	or surface prot	or surface prot	hypothetical prote		-	FmtB protein [impo	hypothetical prote	fibrinogen-binding	hypothetical prote	hypothetical prote	hypothetical prote	subtilisin-like pr	protein - 1	ble oute	surface membrane p	l protein - Myc	toxin-like outer m	probable autotrans	ser-lys rich hypot	hemagglutinin homo	probable invasin Z	phage-related prot	toxin-like outer m	hypothetical prote
Des	ma j	major	major	major	her	major	major	hyp	sur	hyE	Fmt	hyp	fir	hyE	hyr	hyE	Sut	lmpl	pro	Sur	lmp1	ç	pro	sei	hen	pro	pha	ŝ	hyĘ
QI QI	S48754	548753	S48751	S48752	A49218	S48755	S51560	B89921	JC6009	AG2422	D90011	C89921	S41539	B71605	A86827	F82885	S44131	T30822	D71850	PC6003	T18351	H71879	AC0976	T40462	B49218	E85822	F96907	D71917	AG2560
DB	1	7												•	~													~	
Length	702	702	650	649	647	386	320	6713	1302	661	2481	3890	933	807	1072	4688	682	1365	1237	624	1051	2399	1107	751	135	2660	1645	3194	1487
% Query Match	41.6	37.7	37.2	37.2	35.7	28.8	9.5	8.8	8.7	8.3	8.2	8.2	8.0	7.8	7.8	7.8	7.7	7.7		•	•	•	•	•	7.1		•	7.0	7.0
Score	831.5	~	744	743	713	575.5	189.5	175			164.5	163.5	159	156	155	155	2	5	151.5	151	150.5	145	14	143.5	142	4	41.	4	139.5
Result No.		7	e	4	ņ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

rhoptry protein -	transcription regu	cell surface antig	conserved hypothet	fibrinogen-binding	surface layer prot	filamentous hemagg	hypothetical prote	membrane associate	kinesin-related pr	hypothetical prote	hypothetical prote	kinesin-like prote	hypothetical prote	rhoptry protein -	hypothetical prote
T28676	TNBYR6	T17519	AE1130	D89852	S68553	T31102	S55119	E97066	S14032	F90073	F82884	T38378	A64596	T28677	B97806
7	-	~	7	~	7	7	7	~	~	7	7	~	7	7	7
2401	1314	820	926	686	1524	4152	719	568	1073	2271	5005	1085	1238	2269	589
7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.9	9.9	9.9	9.9	9.9	9.8	9.9	9.9	6.7
139.5	138.5	137.5	137.5	137.5	137.5	137.5	137	136.5	136.5	136.5	136	135.5	135.5	135	134.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 S48754 major surface protein (clone pMGA1.4) precursor - Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 C; Accession: S48754	
	PW. M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Brownir -352, 1994 sation of the multigene family which encodes the major cell S48751; MUID:95010739	ıg, G.F surfac
	A; Accession: 348754 A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: DNA	
	A; Kesiques: 1-702 cmAr> A; Coss-references: EMBL:L28424 C; Genetics:	
	A;Genetic code: SGC3 A;Start codon: GTG	
	Query Match 41.6%; Score 831.5; DB 2; Length 702; Best Local Similarity 42.0%; Pred. No. 3.2e-38; Matches 173; Conservative 84; Mismatches 116; Indels 39; Gaps 8;	
	QY 8 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 61 :	
	Qy 62 NLNATLEQLKMAKTNLESAINQANTDKTTFPDNEHPNLVEAYKALKTTLEQRATNLEGLSS 121 :	
	QY 122 TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA 181 :	
	QY 182 DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235	
	Qy 236 WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVK 290 :	
	Qy 291 AADANNVGLOYKLNNGNVQQVEFATSTSANNTTANPTPAVD 331 :: :: : :: :: Db 366 SSDSDKVALEYKLNESAVKTIDFSPSQTSPVASDATRENNRSTAAPAQGSTEINPAPTLD 425	
-	Qy 332 EIKVAKIVLSGLRFGONTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK 382 	

40;

Length 650;

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major surface protein (clone pMGA1.2) precursor - Mycoplasma gallisepticum (c;Species: Mycoplasma gallisepticum C;Species: Mycoplasma gallisepticum C;Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 C;Accession: 548752 M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F. R;Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F. A;Tile: The organisation of the multigene family which encodes the major cell surface A;Reference number: $48751; MUID:95010739
A;Cross-references: GB:U90714; EMBL:L28423; NID:g1905869; PIDN:AAB50152.1; PID:g19058 R;Markham, P.F.; Glew, M.D.; Brandon, M.R.; Walker, I.D.; Whithear, K.G. Infect. Immun. 60, 3885-3891, 1992 A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Reference number: A44793; MUID:92363591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: L28424; NID: 9535687; PIDN: AAA62416.1; PID: 9535689
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NPNNGQ------TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.2%; Score 743; DB 2; Length 64
42.3%; Pred. No. 2e-33;
live 62; Mismatches 125; Indels
                                                                                                                                                                                                                     A;Note: sequence extracted from NCBI backbone (NCBIP:111017) C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 LRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-649 <MAR>
                                                                                                                                                                                                                                                                                                                                                  Score 744; DB 2;
Pred. No. 1.8e-33;
2; Mismatches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.2%; Scor
42.9%; Pred
tive 62; 1
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Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 26-42 <MA2>
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A; Start codon: GTG
                                                                                                                      A;Contents: S6
A;Accession: A44793
A;Status: preliminary
                                                                                                                                                                                                                                                                            SGC3
                                                                                                                                                                                                                                                                          A;Genetic code: SG
A;Start codon: GTG
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Best Local 5
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                                                                          June 1932 Strate protein (clone pMGA1.3) precursor - Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Species: Mycoplasma gallisepticum C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 (C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999 (C; Accession: S48753 M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994 M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994 M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994 M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F.; FEBS Lett. 352, 347-352, 1994 M.D.; Sylolocy Febs M.S. Residues: J.702 cwaRR> A; Residues: G; Genetic Code: SGG3 A; Conetic Code: SGG3 A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 ANNVGLQYKLNNGNVQQVEF----SAN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTTANPTPAVDEIKVAKIVLSGLRFQQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP----VNYKYARRTVW 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 NGD--EPSSRILANTN-SITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAAD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 SSSVALOYSLNKTSSKLINFKPAETVSTNTDQSENEVATTSTTEARSSYKVLVADEAATS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIRNNLVDLYNKASSLITKTLDPLNG--GTLLDSNEITTANKNINNTLS--TINEQKTNA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.7%; Score 754; DB 2;
41.6%; Pred. No. 5.6e-34;
tive 62; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.7
Best Local Similarity 41.6
Matches 176; Conservative
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283

438

11;

Gaps

48;

Length 649;

QY 8 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60	278 STGYLYEPYKLVKAADANNVGLOYKLNNGNVQQVEFATSTSANNFTANPTPAVDE 33
Qy 61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120 	Db 338 STGYLYFPYKLVNTSDQVKLGLEYKLNDATKPSAITFGSDQTMNGKTPTVND 389 Qy 333 IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQK	390 INVAKVTLANLNEGSNKIEFSVPAEF
168 DAQYACIKMHLSGLYDAGKAITTKTLEPVEGDP-LTASAVMMANTKIVEAIKDEVLNPQK 170 maarak gaggetavataansogenyomenaaranooganyomaga aummiy-	
QY 1/9 TRADALSHSFIARVIQUNEQSFYGIFINANVQPSNISFYAFSADVIPVNIKI 230 	major surrace protein (clone pMcAl.s) precursor - Mycopiasma gallisepticum (fragment) C:Species: Mycopiasma gallisepticum C:Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
QY 231 ARRIVW-NGDEPSSRILANTNSITDVSWIYSLAGTNTKYOFSFSNYQPSTGY 281 1: : :: : :	C. Arcession 347. Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F FEBS Lett. 352, 347-352, 1994 A.Title: The organisation of the multigene family which encodes the major cell surface.
Qy 282 LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVA 336	A; Reterence number: 540/31; MULD:930LU/39 A; Accession: 84875 A; Status: preliminary; nucleic acid sequence not shown A; Molecule type: DNA
Qy 337 KIVLSGLRFGQNTIELSVPTGEGNWNKVAPMIGNIYLSSNENNADKI 383 	A.Residues: 1-386 <mar> A.Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62419.1; PID:9535692 A.Note: the sequence of residues 385-386 and the corresponding nucleotide sequence ar</mar>
RESULT 5	A;Start codon: GTG
A49218 hemagglutinin homolog pMGA1.2 - Mycoplasma gallisepticum C;Species: Mycoplasma gallisepticum C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999	Query Match 28.8%; Score 575.5; DB 2; Length 386; Best Local Similarity 42.3%; Pred. No. 1.5e-24; Matches 138; Conservative 50; Mismatches 113; Indels 25; Gaps 10;
Arctesion: 449-40. M.D.; Whithear, K.G.; Walker, I.D. Infect. Immun. 61, 903-909, 1993 A:Title: Molecular clonding of a member of the gene family that encodes pMGA, a hemagglut	OY 8 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 61
A: Accession: A49218 A: Status: preliminary A: Molecule type: DNA: protein	QY 62 NLMATLEQLKMAKTNLESAINQANTDKTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 121
A; KESIQUES: 1-04, CMAKA. A; CROSS-references: GB: S55216; NID: 9265625; PIDN: AAB25397.1; PID: 9265626 A; Experimental source: S6 A; Note: sequence extracted from NCBI backbone (NCBIN: 125182, NCBIP: 125183)	QY 122 TA-YNQIRNNLVDLYNKASSLITKTLDPLN-GGTLLDSNEITTANKNINTLSTINEQ 177 :
C; Genetics: A; Genetic code: SGC3	QY 178 KTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNY 228
Query Match 35.7%; Score 713; DB 2; Length 647; Best Local Similarity 41.1%; Pred. No. 8.8e-32; Matches 169; Conservative 60; Mismatches 124; Indels 58; Gaps 12;	OY 229 KYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS-TGYLYFPYK 287 : : : : : : :
QY 8 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60	288 LVKAADANNVGLQYKLNNGNVQQVEF 313
QY 61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120 : :: :	DD 361 LVQINDNVGLQIVLNNTIPKLVNF 384 RESULT 7
QY 121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEGK 178 168 DAQYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTASAVMMANTKIVEAIKDEVLNPQK 226	S21300 R. Species: Mycoplasma gallisepticum C;Species: Mycoplasma gallisepticum C;Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
QY 179 TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV 226	C;Accession: Silbou; S48/5/ R;Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, G.F FEBS Lett. 352, 347-352, 1994 A;Title: The organisation of the multigene family which encodes the major cell surfac
QY 227 NYKYARRTVW-NGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGP 277 :	A;Reterence number: 548751; MUID:95010739 A;Accession: 551560 A;Status: nucleic acid sequence not shown A;Molecule type: DNA

sys

gene

```
A; Genetic code: SGC3
C; Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homolo C; Superfamily: surface-located membrane protein
C; Keywords: duplication; membrane protein [Lmp3] #status predicted <SIG>F; 1-24 / Domain: signal sequence #status predicted <SIG>F; 25-1302/Product: surface-located membrane protein [Lmp3] #status predicted <MAT>F; 957-992//Domain: tetratricopeptide repeat homology <TT1>F; 1089-1120//Domain: tetratricopeptide repeat homology <TT2>F; 1089-1120//Domain: tetratricopeptide repeat homology <TT3>F; 1154-1190//Domain: tetratricopeptide repeat homology <TT4>F; 1150///Fitatricopeptide repeat homology <TT4>F; 1150///Fitatricopeptide repeat homology 
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hypothetical protein all4935 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AG2422
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Ix
                                                                                                                                                                                                                                                                                                      C; Species: Mycoplasma hominis
C; Species: Mycoplasma hominis
C; Date: 10.5ep-1999 #sequence_revision 10.5ep-1999 #text_change 21-Jul-2000
C; Accession: JG6009
R; Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. J. Bacteriol. 176, 275-2784, 1996
A; Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp A; Reference number: JG6009; MuID:96213016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1302 <LAD>
A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVA
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                                                                         886 LOGAINDKDATLRNONYLDADES
-----KVAPMIGNIYLSSNEN
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Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: lmp3
Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #text_change 22-oct-2001
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Accession: B89921
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; C; Shiba, T.; Hattori, M.; Ogaswara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Residues: 1-6713 <KUR>
A;Cross_references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
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                                                       PID:9535688
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                                                                                                                                                                                                                                                                                   Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6713;
                           A;Cross-references: EMBL:L28424; NID:g535687; PIDN:AAA62415.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.8%; Score 175; DB 2; Length 67 Best Local Similarity 22.6%; Pred. No. 0.54; Matches 100; Conservative 66; Mismatches 179; Indels
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                                                                                                                                                                                                                                                                               ; Score 189.5; DB 2;
; Pred. No. 0.0015;
11; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 ELSVP-TGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.5%;
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.9%
Matches 46; Conservative
                      A; Residues: 1-320 <MAR>
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                                                                                                                                                            A;Genetic code: SGC3
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hypothetical protein ebbB [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
C;Accession: C89921
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, L.; Antori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A;Reference: DNA
A;Residues: 1-3890 <KUR>
A;Residues: 1-3890 <KUR>
A;Residues: 1-3890 <KUR>
A;Experimental source: Strain N315
C;Genetics: A;Genetics: A;Ge
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                                                                                                                                                                                                                  1410 AQTTN------DVTQI------KDQAVADIQGITADTTIKDVAKDELAT 1446
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                                                                                             1186 DQAKTTGETSIDQVTPTVNKKATARNEITAILNNKLQEIQATPDATDEEKQAADA--EAN 1243
                                                                                                                                                                       58 TVNNNLN-----ATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTL-- 109
                                                                                                                                                                                                                                                                                                                       110 -EQRATNLEGLS-----STAYNQIRNNL------VDLYNKASSLITKTLDPLNGGTLL 155
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                       DANPINICOTOLE-----AARMELTDLINAKAMTLASLODYAKIEASLSSAYSEAE
                                                                                                                                                                                                                                                                                                                                                                      156 DSN-----EITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 NTKYQFSFSNYGPSTGYLYFPYKLVKAADAN------NVGLQYKLNNGNVQQVEFATST
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2422
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C; Species: Staphylococcus aureus
C; Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D90011
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Molecule type: DNA
A;Residues: 1-2481 <KUR>
A;Coss-references: GB:BA000018; PID:g13701961; PIDN:BAB43253.1; GSPDB:GN00149
A;Experimental source: strain N315
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A;Molecule type: DNA
A;Residues: 1-661 <KUK>
A;Residues: 1-661 <KUK>
A;Cross-references: GB:BA000019; PIDN:BAB76634.1; PID:g17134073; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.3%; Score 165.5; DB 2; 22.7%; Pred. No. 0.082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Mismatches 188;
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Length 3890; Indels

Gaps

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RESULT 15
A86827
hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL140 c; Species: Lactococcus lactis subsp. lactis
C; Date: 23 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Date: 23 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C; Accession: A86827
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
A; Title: The Complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A86827
A; Accession: A86827
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-1072 csroo>
A; Cross-references: GB: AE005176; PID: 912724625; PIDN: AAK05715.1; GSPDB: GN00146
A; Experimental source: strain IL1403
A; Genetics:
A; Genetics:
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71605
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule type: DNA
A;Residues: 1-807 <GAR>
A;Residues: 1-807 <GAR>
A;Residues: 1-807 <GAR>
A;Cross-references: GB:AE001420; GB:AE001362; NID:g3845287; PIDN:AAC71959.1; PID:g384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||::| |||| | :: | |||| | 468 INNNISYT--QLKMNNINFNIHMESPINQQHNNTFKVNNDTNFFNEPTNKKKKNKEKK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    687 VNNMNNPMYFPNVNIQ-KDDSNIALLYNNKPNIDFNNFQLNHINNHMIQNNIMTNNVMLN 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVT 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 YGPSTGYLYFPYKLVKAADANNVGLQYK------LUNGNVQQVEFATSTSAN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VNNNLNATLEQLKMAKT----NLESAINQA--NTDK----TTFDNEHPNLVEAYKALKT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            575 QKKHNKMSQVSKQSNNKNNKNNSHLKKQININ-----TNNNMDNKNNSHISKNVIVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
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21.0%; Pred. No. 0.59;
tive 76; Mismatches 154; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSE-AETVNNNL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 156; DB 2; Length 80; Pred. No. 0.35; 48; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.8%;
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Best Local Similarity 21.0%
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.88
Matches 73; Conservative
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746 NNLTTSN 752
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C: Species: Staphylococcus aureus
C: Species: Staphylococcus aureus
C: Species: Staphylococcus aureus
C: Accession: 841539; 836630
R: McDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.
Mol. Microbiol. 11, 237-248, 1994
A: Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staphy. Reference number: 841539; MUID: 94224142
A: Accession: 841539
A: Accession: 841539
A: Accession: 841539
A: Accession: 841539
A: Status: pre-liminary
A: Molecula type: DNA
A: Residues: 1-933 < MCD>
A: Residues: 1-933 < MCD>
A: Cross-references: EMBL: 218852; NID: 9397525; PIDN: CAA79304.1; PID: 9397526
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                                                                                                                                                                                                                                                                                                           3783 DQAMAN------LQNGINNESQVKSSEKYRDADINKQQEYDNAITAAKAILNKSTGPNT 3835
                                   NNDKQTAYNNAVAAAETIINANSNPEMNPSTITQKAE--QVN---SSKTALNGDENLATA 3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                               KAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDE-IKVAKIVL---SGLRF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TTNQANTPATTQSSNTNAEELVNQ-TSNETTFND--TNTVSSVNS-----PQNSTNAENV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SST-----AYNQIRNNLVDLYNK------ASSLITKTLDPLNGGTLL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSNEITTANKNINNTLSTINEQ----KTN-ADALSNSFIK----KVIQNNEQSFVGTFTN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ||: :||| :||: ||----|
----IMAGDQ----VLANGVIDSDGNVIYTFTDYVN 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 PTPAVDEIKVAKI-----VLSGLRFGQNTIELSVPTGEGNMNKVAPMI-GNIYLSSNE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 KTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTYRQTIYVNPSGDNVIAPVLTGNLKPNTDS 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
B71605
hypotheticąl protein PFB0850c - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 -INQLINVIVGIDSGTTVYPHQAGYVKLNYGFSVPNSAVKGDIFKITVPKELNLNGVTST
                                                                                                          241 -PSSRILLANT-NSITD-----VSWIYS---LAGTNTKYQFSFSNYGPSTGYLYFPYKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 STTQDTSTEATPSNNESAPQSTDASNKDVVNQAVNTSAPRMRAFSLAAVAADAPAAGTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 ANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG-TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 159; DB 2; Length 933; 22.8%; Pred. No. 0.29;
                                                                                                                                                         57; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrinogen-binding protein - Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :| : | | : | 3836 | 3836 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 3861 | 
                                                                                                                                                                                                                                                                                                                                                                                                                 GONTIELS --- VPTGEGNMNKVAPMI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKVPP---
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3 ESNSVSDQTSSEAS-TNSNSSISLSPSNISSTSDSESATNSSDFSNVAEVANNSLASV 486	64 -NATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATN		5EEG-LSSTAYNQIRNNLVDLYNKASSLITKTLDPLN	547 SPSNISSTSVLESTTSSSNFSNVAEVANNSLASVNNSSSSVLSSTSTADNLEINQFGSDN 606	153 TLLDSNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPS	TINDESELSTSGAFLSSNQTSSEASSNSMSSINSPSLSLSLSNSES	NYSEVAESADVIPONYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLAG	MQSNSSEATKVDNNSSTHSSNILNSGSNDSSDSDSDSDSDSSSNLSSSPN 704	I TNTKYQESFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLANGNVQQVEFATSTSANNT	LETNQTISSTPSEVNISTPUTIS	3TANPTPAVDELSVPTGEG	HEMSTNPKSSISSPISTISSSQQKESQSNLLNTTEGINNPITFNNSSSENSAASILTSYS	360 NWNKVAPWIGNIYLSSINENADKI 383	NNNSESSETGCLYISNEAQRDNGSEISHSLPSSNSNENNVSSI 843
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Search completed: June 12, 2002, 10:49:47 Job time: 205 sec

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Sequence 34,
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Sequence 2, A
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Sequence 15,
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Sednence:

Title:

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Searched:

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APPLICANT: Saito, Shuji
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Funato, Hirono
APPLICANT: Iritani, Yoshikazu
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBIRANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBIRANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND ADDRESSEE: NAUGHTON
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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US-08-242-932-2
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US-08-169-27-2
US-09-336-447A-15
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US-09-669-974-33
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-194
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND, LE-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1725 K Street, Suite 1000 CITY: Washington
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APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-5EP-1995
CLASSIFICATION: 424
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                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-125-742-4
US-08-225-742-2
US-09-421-992A-8
US-09-541-782-6
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US-09-268-347-30
US-08-923-992A-4
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Result

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PatentIn Release #1.0, Version #1.30
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; Pred. No. 3.4e-128;
10; Mismatches 7;
                                                                                                                                                                                                      FALCATION NUMBER: PCT/UP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLEJAND, LE-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELEDRIONE: 202-659-2930
                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: PCT/JP94/00541
                                  UMBER: US/08/525,742
25-SEP-1995
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Patent No. 5871742
GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Oheawa, Ikuroh
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Ohkawa, Setsuko
Saeki, Sakiko
Ohsawa, Ikuroh
Funato, Hirono
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                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 610 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 95.59
Matches 365; Conservative
                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                    APPLICATION NUMBER: FILING DATE: 25-SEP
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US-08-525-742-4
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APPLICANT: Onsawa, Ikuroh
APPLICANT: Onsawa, Ikuroh
APPLICANT: Fundach, Hirono
APPLICANT: Fundach, Hirono
APPLICANT: Tritani, Yoshikazu
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           Score 1910; DB 2;
Pred. No. 3.8e-132;
3; Mismatches 4;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                           Query Match 95.6%;
Best Local Similarity 98.2%;
Matches 376; Conservative
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APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
                                                      LENGTH: 615 amino acids TYPE: amino acid
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LIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy APP

COMPUTER: TPM COMPUTER:
                     INFORMATION FOR SEQ ID NO:
                                     SEQUENCE CHARACTERISTICS
                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-742-10
   202-8870357
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STREET: 17
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301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
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IBM PC compatible
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95.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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US-08-185-851A-4
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          APPLICANT: Takahashi, "Simohito tribe of inventions new Polypeptide, dna encoding the tribe of inventions new Polypeptide, dna encoding the searing the dna and tribe of inventions recombinant virus utilizing the recombinant vector as well number of sequences: 51 correspondence address:
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STREET: 1725 K Street, Suite 1000
STREET: STABELY, WASHINGTON
                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1638; DB 2;
Pred. No. 1.5e-112;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR.1993
PRIOR APPLICATION NUMBER: JP 05-245625
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND, NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%;
95.5%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
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Containing the Gene As
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 CMSITKKDANPNNGQTQLQAARMELTDLINAKARTLASLQDYAKIEASLSSAYSEAETVN 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 368;
                                                                                                                                                                                                                                                                                               APPLICANT: Fujisawa, Ayumi
APPLICANT: Iritani, Yoshikazu
APPLICANT: Aoyama, Shigemi
TITLE OF INVENTION: Poultry Mycoplasma Antigens, Gene
TITLE OF INVENTION: Pullry Mycoplasma Antigers, Gene
TITLE OF INVENTION: Thereof and Recombinant Vectors Cont
TITLE OF INVENTION: Well As Vaccines Utilizing the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS version 5.0 SOFTWARE: ASCII from Word Perfect version 5.1 CURRENT APPLICATION DATA: US/08/185,851A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1612; DB 1;
Pred. No. 1.2e-110;
6; Mismatches 11;
327 YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1725 K Street, N.W., Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36,281
R: PO-8-A930918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Thereas M. Stevens-Smith
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: PO-8-A
TELECOMMUNICATION:
TELECHONE: 202-659-2930
                                                                                                                                                         Sequence 4, Application US/08185851A
Patent No. 5489430
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ω 7	DD 45 NTNPSDGGGMMNAAAKELADAKAALTTLINGETANLASYEDYAKIKSELTSAYETARAVS	OY 61 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVBAYKALKTTLEQRATNLEGLS	121	165	QY 181 ADALSNSFIKKVIQNNEQSFVGFFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE	Qy 241PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD	OY 294 ANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIV	WELL QY 340 Db 401	380	Db 456 PTAVTVDLLKGY 467	RESULT 6	US-08-293-728-2 ; Sequence 2, Application US/08293728D . Patent No. 600831	; GENERAL INCORPOSATI ; APPLICANT: Foster, Ti	; APPLICANT: McDevitt, Damien L. ; TITLE OF INVENTION: The S. aureus Fibrinogen	FILE REFERENCE: 05344.	; CURRENT FILING DATE: 199, ; NUMBER OF SEQ ID NOS: 20 ; SOFTWARE: PATENTIN VOT	; SEQ ID NO 2 ; LENGTH: 933	; TYPE: PRT , ORGANISM: Staphylococcus US-08-293-728-2	Onerv Match	Best John Similarity 22.8%; Matches 96; Conservative 5	6	73	QY 60 NNNLNATLEQLKWAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL : : : : : : :	OY 120 SSTAVNQIRNNLVDLYNK
	267 PSSRILANTNSITDVSXIXSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAA	QY 301 YKLNNGNVQQVEFATSTSANNTTANPTPAVDELKVAK 337		About 3 08-08-525-742-2 ; Sequence 2, Application US/08525742	Patent No. 5871742 GEMERAL INFORMATION: APPLICANT: Saito, Shuji APPLICANT: Ohkawa, Setsuko		A TAYARDA SAIRGENT SAYARDA SAY	TITLE OF INVENTION: EXCOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS TITLE OF INVENTION: AS USE THEREOF UTILIZING THE RECOMBINANT VECTOR AS NUMBER OF SEQUENCES: 51	CORRESPONDENCE ADDRESS: ADDRESSE: AMSTRONG, WESTERMAN, HATTORI, MCLELAND & ADDRESSEE: NAUGHTON	2	SIAIE: DC COUNTR: USA ZIP: 2000	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWADER: DS-DOS-MS-DOS SOFTWADER: DS-DOS-MS-D	36	FILING DATE: 25-EP-1995 CLASSIFICATION: 424	PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 05-074139	FILING DATE: 31-MAR-1993 PRIOR APPLICATION DATA: TP 05-24-625	P K	FILING DATE: 31-MAR PLIJO94/00541 FILING DATE: 31-MAR PLIJON:	NAME: MCLeland, Le-Nhung REGISTRATION NUMBER: 31,541 REFERENCE/DOCKET NUMBER: 950811	TION	ည်း	SEQUENCE CHARACTERISTICS: LENGTH: 661 amino acids TYPO: amino acid TOPO: 11.pag	YPE:

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192 IRKQAQQPDKKEDAEVKVREELGKLFSSTKAGLDQEIQEHVKKETSSEENTQKVDEHYAN 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ITKKDANPNNGQTQLEAARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AE 57
                                                                                                                                                                                                               APPLICANT: Tai, Joseph Y.
APPLICANT: Tai, Joseph Y.
TITLE OF INVENTION: No. 6280738-1gA FC Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 ESLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----
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22.7%; Pred. No. 0.063;
tive 51; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                   Sequence 8, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2610
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 22.7%
Matches 84; Conservative
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MEDIUM TYPE: Floppy
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                                                                                    RESULT 8
US-08-923-992A-8
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                                               ---IMAGDQ-----VLANGVIDSDGNVIYTFTDYVN 324
                                                                                                       266 TKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTAN 325
                                                                                                                                               326 PTPAVDEIKVAKI-----VLSGLRFGQNTIELSVPTGEGNMNKVAPMI-GNIYLSSNE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 DSNEITTANKNINNTLSTINEQ----KTN-ADALSNSFIK----KVIQNNEQSFVGTFTN 206
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Best Local Similarity 22.8%; Pred. No. 0.001;
Matches 96; Conservative 57; Mismatches 154; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUSTALIA DOBA - Application US/09421868

Sequence 2, Application US/09421868

Patent No. 6177084

SCHERAL INFORMATION:
APPLICANT: Foster, Timothy J.
APPLICANT: Foster, Timothy J.
TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene; FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/09/421,868
CURRENT FILING DATE: 1999-10-19
PRIOR FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0
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                                                     292 AKVPP---
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FILE REFERENCE: 1038-860
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| | | | : :|:| : |::|:
611 NGYETLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :|| :| :| | :| :| | :| 671 VSELKDSKNSLLDALEHSLQDISMSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYN 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 YSFVAFSADVTPVNYKYARRTVWNG----DEPSSRILANTNSITDVSWIYSLA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1073;
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                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                    APPLICANT: SAKOWICE, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                    Sequence 6, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: NISLOW, COTEY
                                                 330 VDEIKVAKIV 339
                                                                                  510 OKDSKTEEKV 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 GTNTKYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: S.pombe
US-09-541-782-6
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                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
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GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS

Sequence 24, Application US/09268347 Patent No. 6335182

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 LVDSLNKLGWKVGVGKDGTGATDGTHTDTLVKSGDKVTLKAGDNLKVKQEGTNFTYVLRD 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 KYARRIVWNGDEPS-----SRILANINSIIDVSWIYS---LAGINIKYQFSFSNYG 276
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APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-Iga Fc Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         13 NGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSE-----AET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VNNNLNATLEQLKMAKTNLESA------INQANTDKTTFDN-----EHPN 97
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                                                                                                                                                                                                                                                                                                                                                                                  Indels 175;
                                                                                                                                                                                                                                                                                                                         Length 1002;
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ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     ch 6.6%; Score 132.5; DB 4;
1 Similarity 19.1%; Pred. No. 0.1;
91; Conservative 58; Mismatches 153;
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08923992A
Patent No. 6280738
                                                                                                                                                                                                        ; ORGANISM: Haemophilus influenzae US-09-268-347-24
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 91; Conserva
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                                                                                                                   SEQ ID NO 24
LENGTH: 1002
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Gaps

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416 LSNGLN----FKFKSTDGELLNIKAENDTVTFTPKKGSVQVGDDGKATIQDGAKTTTGL 470
                                                                                                                                                                                                                                                                                                              471 VEASELVDSLINKLGWKVGTGTDGTGVTDGTHTDTLVKSGDKVTLKAGDNLKVKOEGTNFT 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 INNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 NYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 KVAKIVLSGLRFGQNTIEL---SVPTGEGNM-------NKVAPMIGNIYLSSNEN 378
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APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     94 -EHPNLVEAYKAL------EQRATN--
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                                                                                                                                                                                                                                                                                                                                                                                     685 NANE-----VKFKSGNGINVSGKTLDNGTREITFELAKDEN------
                                             51; Mismatches 152; Indels 180;
  6.6%; Score 131; DB 4; Length 1004; 20.2%; Pred. No. 0.13;
                                                                                         13 NGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSEA--
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                                                                                                                                                                              59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTF------DN----
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PAPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Esmond, Robert W.
REGISTRAILON NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                             97; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
Query Match
Best Local Similarity
Matches 97; Conserv
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TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION: NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Mismatches 157;
             CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/024,707
FILLING DATE: 06-5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESENONG, ROBERT W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEPHONE: (202) 371-2540
TELEPHONE: CARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 amino acids
TYPE: amino acids
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Sequence 30, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
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US-09-268-347-30
  05-SEP-1997
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Matches 84; Conservative
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MOLECULE TYPE: protein

US-08-923-992A-2
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548 KDSKTEEKV 556
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LENGTH: 1004
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58 TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE
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GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038 860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENT VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : |: |: | : | : | : 4 | | : 4 | | : 4 | | : 4 | | : 4 | | : 4 | | : 4 | | : 4 | | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | : 4 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 SLEQVEKELKHNSEA-----NLQDLVAKSKEIVREYEGKLNOSKNLP--ELKQLEEEA 364
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ITKKDAN------PNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNTLSTINEQ-----KTNADALSNSFIKKVI---ONNEOSFVGTFTNANVQPSNYSFVAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SADVIPVNYKYARRTVWNGDEPSSRILLANTNSITDVSWIYSLAGTNTKYQFS--FSNYGP
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                                                                                                                                                                                                                                                                                                                                 6.6%; Score 131; DB 4; Length 1104;
20.2%; Pred. No. 0.15;
tive 50; Mismatches 154; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 6.5%; Score 129; DB 4; Length 2048; Best Local Similarity 21.2%; Pred. No. 0.48; Matches 83; Conservative 60; Mismatches 156; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09268347
Patent No. 6335182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-48
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 20.23
Matches 85; Conservative
                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-923-992A-4
                                                                                                                  amino acid
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LENGTH: 2048
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GLSSTAYNQIRNNLVDLYNKA--SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTIN 175
                                                                                                                                                         176 EQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 235
                                                                                                                                                                                                                                                                  236 WNGDEPSSRILANTNSI - - TDVSWIYSLAGTN - - TKYQFSFSNYGPSTGYLYFPYKLVKA 291
                                                                                                                                                                                                                                                                                                                                                                       292 ADANNYGLQYKLNNGNYQQVEFATSTSANNTTANPTPAVDEIKVAKIVL-SGLRFGQNTI 350
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08923992A
Patent No. 6280738
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IGA FC Binding Forms of the Group B
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                     344 AVN-------VAQLEAVVKWAKERRITFQGD-DNSTDVKIGLDNTL----TIK
                                                                                                                                                                                                           438 SSSTTAELLSDSL-----TFTQPN------------
                                                                                                                                                                                                                                                                                                                      457 -TGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDKIGFARDG-DVDEKQAPYLDKKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM ILFL. A-PEL A-L-COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.3%; Score 126.5; DB 4; Best Local Similarity 22.5%; Pred. No. 0.32; Matches 83; Conservative 51; Mismatches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Esmond, Robert W. RECISTRATION NUMBER: 32,893 RECESTRATION NUMBER: 14 REFERENCE/DOCKET NUMBER: 14 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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US-08-923-992A-6
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59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 107
                                                         :||| |: | | || |: : : || || |: :: 359 SLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEEA 359
                                                                                                                                  168 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 219
                                                                                                                                                220 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N 274
                                                                                                                                                                                            410 ------TVYEGEDVKFTVTAKSDSKTTLDFSDLL----TKYNPSVSDRISTN 451
                                                                                                                                                                                                                       275 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 330
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June 12, 2002, 10:47:42; Search time 17.44 Seconds (without alignments) 872.522 Million cell updates/sec
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1998
1 CMSITKKDANPNNGQTQLEA......SSNENNADKIPGYRRPGTFL 393
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                  OM protein - protein search, using sw model
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Perfect score:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

.Searched:

105224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description		٠.	P78586 c arg5,6 pr	P09547 saccharomyc	Q03213 saccharomyc		P47580 mycoplasma		_	Q07833 bacillus su	Q00174 drosophila	P40442 saccharomyc	P32618 saccharomyc	Q12355 saccharomyc		P04933 plasmodium		_	_	P14738 staphylococ	P40957 saccharomyc	P34231 saccharomyc		Q05870 schistosoma	Q09904 schizosacch		P04931 plasmodium	P15293 lactococcus	P46590 candida alb	P80544 staphylococ	P25386 saccharomyc	4	8	Q9pjy2 chlamydia m
SUMMARIES	QI	ATOM COSTA	NISE_LACER	ARS6_CANAL	SWI1_YEAST	YM41_YEAST	CUT7_SCHPO	Y338_MYCGE	BAG_STRAG	RBP2_PLAVB	WAPA_BACSU	LMA_DROME	YIQ9_YEAST	YEF3_YEAST	PST1_YEAST	MSP1_PLAFK	MSP1_PLAFW	P3K2_DICDI	LIN5_CAEEL	YKK1_CAEEL	FNBA_STAAU	MAD1_YEAST	YKS7_YEAST	NSP1_YEAST	MYSP_SCHJA	N124_SCHPO	CAT8_YEAST	ARP_PLAFA	P2P_LACLC	ALS1_CANAL	MRSP_STAAU	USO1_YEAST	FLIC_SALON	YN96_YEAST	PMPB_CHLMU
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	Score	7 7 7	1	143	138.5	137	135.5	132	131.5	129	128.5	128.5	128	127	126.5	126.5	126.5	125.5	124.5	124.5	124.5	124	124	124	124	124	124	123.5	123.5	123	123		122.5	122	122
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P38272 saccharomyc 004893 saccharomyc 054001 salmonella 009625 caenorhabdi P49022 lactococcus P41508 mycoplasma P28742 saccharomyc 00245 equine rota P25146 listeria mo P1685 streptococc P1980 saccharomyc	•
YBYO_YEAST YM96_YEAST TOOLC_SALEN YS8A_CAEEL PIP_LACLA P115_MYCHR RYP1_YEAST P2P_LACPA VP4_ROTEH INLA_LISMO PPAC_STRMU PPAC_STRMU PPAC_STRMU	
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425 1140 491 796 901 1111 1902 776 800 1565)
121.5 121.5 121.1 121 121 121 121 121 120.5 120.5	1
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1

ALIGNMENTS

SULT 1 SP_LACLA	ID NISP_LACLA STANDARD; PRT; 682 AA. AC 007596;	16-OCT-2001 (Rel. 40, Last	(EC 3.4.21).		Bacteria, Firmicutes; Bacillus/Clostridium group;	OC Lactococcus. OX NCBI_TaxID=1360;			RX MEDLINE,93239683; PubMed=8478324;	RA Kuipers O.P., de Vos W.M.;	RT "Characterization of the Lactococcus lactis misin A operon genes		involved in misim biosynthesis."	KL U. BACLETIOI. 1/3:23/6-2366(1993). RN [2]		KC SIKAINOOF3. Pr Mediine=da213458. Dubhad=R161176.		RA Hammelmann M., Entian KD.; RT "Reculation of nicin bioconthesic and immunity in Lactococous lactic	6F3.";	RL Appl. Environ, Microbiol. 60:814-825(1994). RN (3)		RX MEDLINE=95357326; PubMed=7630881; RA Siezen R.I. Rollema H.S., Kuiners O.D., de Vos W.M.		RT and its interaction with the precursor of the lantibiotic nisin.";		CC -!- PATHWAY: LAST STEP OF NISIN BIOSYNTHESIS.	•	CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE	-	CC IN THE REGION OF THE MEMBRANE ANCHOR.	This S	CC between the Swiss institute of Bioinformatics and the EMBL outstation CC the Buropean Bioinformatics Institute. There are no restrictions on i	use by modified	CC entities requires a license agreement (See http://www.isb-sib.ch/announce
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Candida albicans (Yeast).

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13;
                                                                                     InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001209; Peptidase_S8.
InterPro; IPR000209; Peptidase_S8.
InterPro; Pep001809; Peptidase_S8.
PROSTE; PS000136; SUBTILIASE_ASP; 1.
PROSITE; PS00137; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_HIS; 1.
PROSITE; PS00138; SUBTILIASE_SER; FALSE_NEG.
PROSITE; PS001343; GRAM_POS_ANCHORNIG; 1.
Hydrolase; Serine protease; Cell wall; Signal; Transmembrane; Zymogen.
                                                                                                                                                                                                                                                                                                             MEMBRANE ANCHOR (POTENTIÁL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAS SYSTEM (BY SIMILARITY).
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 LRQPLKNQKVEAQPLLISNSSEKKASVYTNSHDFWDYQW------DMKY---VTNNGES 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 KKKRANFVTSSPLIKEKPSNSKDASGVIDNS------ASPLSYRKAKEVVS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSAN---------NT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 YA-LYQPSKKI-----SVGI---IDSGIMEEHPDLSNSLGNYFKNLVPKGGFDNEEPDE 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
ARG5.6 protein, mitochondrial precursor [Contains: N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (N-acetyl-glutamate semilaldehyde dehydrogenase) (NAGSA dehydrogenase); Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-
                                                                                                                                                                                                                                                               NISIN LEADER PEPTIDE PROCESSING SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 TANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIG-NIYLSSNEN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 TGNPSDIVD------KMGHGTEVAGOITANGNILGVAPGITVNIYRVFGEN 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---WNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 682;
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                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                         -> T (IN REF. 2).
D5F29313F2983EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 154.5; DB 1; 21.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                857 AA
                                                                                                                                                                                                                                                                                 PROTEASE NISP.
email to license@isb-sib.ch).
                                                                                                                                                                                                                                     POTENTIAL.
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                           EMBL; L11061; AAA25200.1; -. EMBL; X76884; CAA54210.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.7
Best Local Similarity 21.0
Matches 75; Conservative
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679
682
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                                                          HSSP; P29600; 1GC
MEROPS; S08.059;
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ACT_SITE
ACT_SITE
DOMAIN
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DOMAIN
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                               Microbiology 143:297-302(1997).

-!- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+) + phosphate = N-acetyl-5-glutamyl phosphate + NADPH.

-!- CATALYTIC ACTIVITY: ATP + N-acetyl-L-glutamate = ADP + N-acetyl-L-glutamate 5-phosphate.

-!- PATHWAY: SECOND AND THIRD STEPS IN ARGININE BIOSYNTHESIS.

-!- SPACELLULAR LOCATION: Mitcochodrial.

-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.

-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NAGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ASSLITKTLDPLNGGTLLDSNEITTANKNIN-NTLSTINEQKTNADALSNSFIKKVIQNN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NSITD-----VSWIYSLAGTNTKYQFSFSNYG-PSTGYL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 K----TTFDNEHPNLV-EAYKALKTILEQR-----ATNLEGLSSTAYNQIRNNLVDLYNK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 IEASLSSAY----SEAETVNN---NLNATL------EQLKMAKTNLESAINQANTD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 VEAAINSGYLPILTSLAETSSGOLLNVNADVAAGELAREFEPLKIVYLNEKGGIINGNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKVSAINLDEEYEDLLKESWVKYGTKLKIKEIHDLLQHLPRSSSVA-----IIDVNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 QKELFTDS----GAGTL-----IRRGYRLINRNSLRDFG----NPDLLRNALLR----
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                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 64385 / 1001;
MEDLINE=97195775; PubMed=9043106;
Negredo A., Monteoliva L., Gil C., Pla J., Nombela C.;
Negredo, a., Monteoliva L., Gil C., Pla J., Coning, analysis and one-step disruption of the ARG5,6 gene of Candida albicans.";
            Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Mismatches 134; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00696; aakinase; 1.
Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF01774; Semialdhyde_dhc; 1.
ProDom; PD003765; AGPR_act_site; 1.
PROSTITE; PS01224 ARGC; 1.
Oxidoreductase; Transferase; Kinase; Arginine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 143; DB 1; Length 857; 23.3%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion; Multifunctional enzyme; Transit peptide.
TRANSIT 1 7 MITOCHONDRION (POTENTIAL).
CHAIN 7 7 ACETYLGLUTAMATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE2CEAD8FF8C4C71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000706; AGPR act_site.
InterPro; IPR001048; Aakinase.
InterPro; IPR000534; Semialdh_dh.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.2
Best Local Similarity 23.3
Matches 99; Conservative
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857 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Transcription regulatory protein SWII (SWI/SNF complex component SWII)
(Transcription regulatory protein ADR6) (Regulatory protein GAM3).
ADR6 OR SWII OR GAM3 OR YPL016W OR LPAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89057455; PubMed-3143101; O'Hara P.J., Horowitz H., Eichinger H., Young E.T.; Throwitz H., Eichinger H., Young E.T.; Throwitz H., Eichinger H., Young E.T.; Throwitz H., Eichinger Domopolymeric amino acid sequences and a potential metal-binding domain."; Nucleic Acids Res. 16:10153-10170(1988).
 ---KLVKAADANNVG--LQYKLNNG---NVQQVE-FATSTSANNTTANPTP 328
                                                                   AVDEIKVA---KIVLSGLR--FGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                          BESIS/ASSIGNED.

FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF
COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
OF GENES. THIS COMPLEX ALTERS CHOMATIN STRUCTURE TO FACILITATE
BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACILITATE
SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Activator; DNA-binding; Nuclear protein; 21nc-finger.
                  Peterson C.L., Herskowitz I.; "Characterization of the yeast SWI1, SWI2, and SWI3 genes, which encode a global activator of transcription."; Cell 68:573-583(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 65 ASN/THR-RICH.
337 385 GLN-RICH.
1241 1258 C4-TYPE.
1314 AA; 147938 MW; F442D5A82013CDBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                     PRT; 1314 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE-92154671; PubMed-1339306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, U33335, AAB68089.1; -.
EMBL, X12449; CAA31013.1; -.
PIR, SO5728; TNBYR6.
TRANSPRC, T01279; -.
SGD, SO005937; SW11.
Interpro; IPR001606; ARID.
PF031388; ARID; 1.
SMART; SM00501; BRIGHT; 1.
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-4932;
                                                                                                                                           384 PGYRR 388
                                                                                                                                                                              QGYNK 579
283 YFPY---
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P09547;
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SEQUENCE
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                                                                                                       57 NINNNINITURGASGVD------DEQNFEDPKPFDQNLDSNNNNSNSNNNDNNNS--N 104
                                                                                                                                                                                      105 TVASSTNFTSPTAVVNNAAPANVTGGKAANFIQNQSPQFNSPYDSNNSN----TNLNSL 159
                                                                                                                                                                                                                                                DEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVG 298
                                                                                                                                                                                                                                                                                                                                                                                                                 248 NLTSNQLISN-----SDNNNNS 285
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                                                                        10 NPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQ
                                                                                                                                                70 LKMAKTNLES---AINQANTDKTT-----FDNEHPNLVEAYKALKTTLEQRATNLEGL
                                                                                                                                                                                                                           SSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKT
                                                                                                                                                                                                                                                                                                                       2 MSITKKDANPNNGQTQLEAARMELTDL------INAKAMTLAS-----
                                                                                                                                                                                                                                                                                                   180 NADALSNSFIKKVIQNNEQSFVGTFTNANVQP-SNYSFVAFSADVTPVNYKYARRTVWNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.9%; Score 137; DB 1; Length 719;
19.8%; Pred. No. 1.1;
tive 72; Mismatches 175; Indels 178;
 Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 79-4 kDa protein in ALD2-DDR48 intergenic region.
WR172W OR YM8010.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGUENCE FROM N.A.
STRAIN=S288C / AB972;
STAIN=S288C / A. Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4652BE93743D5A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 NNHNMRNNSNNKTSNNNNVTAVPAATPANTNNSTSNANTVFSE 328
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 LOYKL-----NNGNVQQVEFATSTSANNTTANPTPAVDE
6.9%; Score 138.5; E
20.4%; Pred. No. 1.9;
:1ve 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
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                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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               Similarity
70; Conserv
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 Query Match
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                   Best Local
Matches 7
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YM41_YEAST
                                                                                                                                                                                                                                                                                                                                                                            239
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-1-FUNCTION: COULD BE A SPINDLE POLE BODY WOTOR. ON TRANSITION FROM
G2 TO M PHASE OF THE CELL CYCLE, THE SPINDLE POLE BODY DUPLICATES;
THE DAUGHTER POLE BODIES SEED MICROTUBÜLES WHICH INTERDIGITATE TO FORM A SHORT SPINDLE THAT ELONGATES TOSPAN THE NUCLEUS AT
METAPHASE. MUTATIONS AT CUT7 BLOCK SPINDLE FORMATION.
-1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335
                                                                       97 LLRTSAAISAPTGTSQPTETIGEKLSNEERVNSNVSASNSTTAGTGRMLSQSLTN-DSPS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hagan I., Yanagida M.;
"Novel potential mitotic motor protein encoded by the fission yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 NDHASAAQKPISALSPLINSHNSTISMNYINSSIHSGVISASNSFHDLNSLNNFGTITAL
-----SLSSAYSEAETVNNNLNA-----TLEQLKMAKTNLESAI
                                                                                                                                                                                               216 KLVAQPSARPSTNNAQNKLAIELLNSISAVSSAYLQKMQNNGSGRQHTADLCTGDSNTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------DALSNSFIKKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 GINQHRTTNGTIDVNTNTAQLNNQFSNALNTILPDQQHNRNNVSQNINQSLPNRQLGPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QNNEQSFV-GTFTNANVQPSNYSFVAFSAD----VTPVNYKYARRTVWNGDEPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 NTQANQNQSQVLIHNTNTHQQVNRSPISEPNASTDKPFKLNPNGIKRRRNTQSNNNAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SRILANTNSITDVSWIYS-----LAGTNTKYQF-SFSNYGPSTGY
                                                                                                                                                                                                                                                                                                           ----NGTLDSNEITTANKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456 SLPSLALDNASFPPNQNVIPPIINNTQQPLSFSQLINQDSTTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 GLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRPGT 391
                                                                                                                                                   NQANTDK - - - - TTFDNEHPNLV - - - EAYKALKTTLEQRATNLEGLSSTAY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast)
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1992 (Rel. 21, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------INNTLSTINEQKTNA------
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-LQDYAKIEA--
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                                                                                                                                      PRINTS; PRUDJOSC, DESCRIPTION OF PROBLEM STATES SMARTS; SMOLD29; KISC; 1.

PROSITE; PSG00411; KINESIN_MOTOR_DOMAIN1; 1.

PROSITE; PSG0067; KINESIN_MOTOR_DOMAIN2; 1.

MATCOR protein; Cell division; Macrotubules; ATP-binding; Coiled Coil; Mitosis; Cell Givision; Macrotubules; Repeat.

DOMAIN 70 KINESIN-MOTOR (BY SIMILARITY).

DOMAIN 436 604 COILED COIL (POTEWTIAL).

DOMAIN 715 740 COILED COIL (POTEWTIAL).

DOMAIN 715 740 COILED COIL (POTEWTIAL).

DOMAIN 715 740 COILED COIL (POTEWTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 GTNTKYQ--------PSFSNYGPSTGYLYFPYKLVKAADANNVGL--QYKLNNGNVQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 QVE----FATSTSANNTT-----ANPTPAVDEIKVAKIVLSGLRFGQNTI---- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   623 NGYFTLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LEQLKMAKTNLESAINQANTDKTTFDNEHPN----LVEAYKALKTT---LEQRATNLEG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 NGQ-TQLEAARMELTDLINAKA-MTLASL----QDYAKIEASLSSAYSEAETVNNNLNAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906 GVNLEVQTLDRLLQKVKEHSEDNTKEKHQQL---LDLLESLVGNNDNLIDSIKTPHTELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 YSEVAFSADVIPVNYKYARRIVWNG----DEPSSRILANTNSITDVSWIYSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             854 ----ASQAEIVGANKERIQKTVENGSQLLDSKSKAIHSNSRSMYD----HCLALAESQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%; Score 135.5; DB 1; Length 1085; 20.9%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                               LRAILGNDVSLLLLTL (IN REF. 1). W; 5669277875559D58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
SASNPRKRREPPTIDTGYPDRSDTNSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 2.2; 76; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG338 precursor.
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or send an email to license@isb-sib.ch)
                                              EMBL; 270691; CAA94636.1; -. PIR; S14032; S14032. HSSP; P17119; 3RAR. InterPro; PFR001752; kinesin. Pfam; PF00225; kinesin; 1. PRINTS; PR00380; KINESINHEAVY.
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(Rel. 33, Last sequ
(Rel. 40, Last anno
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                                  EMBL; X57513; CAA40738.1;
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                                                                                                                                                                                                                                                                                                                                                                                               61
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97; Conserv
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01-FEB-1996
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P47580;
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SIT--DVSWIYSLAGTUTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNV 308
                                                                                                                                                                                                                                                   Streptococcus.
NCBI_TaxID=1311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1164
                                                                                                                                                            01-AUG-1992
01-AUG-1992
                                                                                                                                     BAG_STRAG
P27951;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucler T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANK--NINNTLSTIN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 GTSSNL-----NPLDKFIKSSSATTVMMK----SAMTKSQEVTSDNNGFNVKSEFLKIN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLSSSGSDNSSNTQSFWKQVQALNNSSQTATIFDAVRMESNSSQAQVVTSNLLVSLSSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 VTPVNYKYARRIVW-NGDE-----ILANIN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E--QKTNADALSN--SFIKKVIQNNEQSFVGTFTNANVQPSNYS------FVAFSAD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 TT---QKQQQKPVYVRGDDAIYAFHIDGGNYFLENSSPNKRNFEKQAEVLLMRFLQGQTN 532
                                                                                                                                                                                                                                                                                       sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAK-IEASLSSAYSEAETVNNNLNA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                   STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                  Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                            (Potential).
SIMILARITY: BELONGS TO THE MG307 / MG309 / MG338 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL LIPOPROTEIN MG338.
N-ACYL DIGLYCERIDE (POTENTIAL).
W; FCE6042067310A70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.6%; Score 132; 22.2%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                 STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142492 MW;
                                                                                                                                                                                                                         SEQUENCE OF 1023-1114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U39715; AAC71563.1; -.
                                                                                                                                                                                                Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U01809; AAD12341.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26
1271
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             qenitalium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1271 AA;
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                                             NCBI_TaxID-2097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; MG338;
           Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPID
SEQUENCE
                                                                       SEQUENCE
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Matches 8
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EXTRACELLULAR (POTENTIAL).

MEMBRANE ANCHOR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

IGA-ENDING (POTENTIAL).

IGA-BINDING (POTENTIAL).

IGA-BINDING (POTENTIAL).

PRO-RICH REPEATS.

CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jerlstroem P.G., Chhatwal G.S., Timmis K.N.; "The IgA-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two binding regions:";
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS.
fw: 65DE94AF720A5474 CRC64;
                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19A FC receptor precursor (Beta antigen) (B antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Repeat; Signal;
                                                                                                                                                                                                                                                      1164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Cell wall; Transmembrane; Receptor; Repe.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S15330; FCSOAG.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00746; Gram_pos_anchor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=LA239;
MEDLINE=91312121; PubMed=1857207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION OF IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 5:843-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA; 131051 MW;
                                                                    309 QOVEFATSTSANNTTANPT 327
                                                                                                                     584 DVCDLAKKLLKNNTNLSET 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X59771; CAA42442.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae.
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1164
1131
1159
1164
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Gaps

Indels 122;

Mismatches 140;

70;

Conservative

89;

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Matches
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                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
-1- SUBCELLULAR LOCATION: Membrane-bound (Probable).
                                                                                                                                                                                                                                                                                                                    TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| | : | | | : | | | | : | | 389
                                                                                                                                                                                                                  ----VEAYKALKT 107
                                                                                                    6 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 58
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                        345 SLEQVEKELKHNSEA------NLEDLVAKSKEIVREYEGKLNQSKNLP--ELKQLEEEA
                                                                                                                                                                                                                                                                                                                                                                                                                               NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF
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Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1251 1251
1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                                        Indels
     DB 1;
                                                        157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                     59 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1251 AA
6.6%; Score 131.5; E
22.8%; Pred. No. 3.9;
ive 51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galinski M.R., Medina C.C., Ingravallo P., "A reticulocyte-binding protein complex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last annotation upda
Reticulocyte binding protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-92315338; PubMed=1617731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium vivax (strain Belem)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Membrane.
                              22.8%;
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                                                          84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          merozoites.";
Cell 69:1213-1226(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 DEIKVAKIV 339
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                                    Similarity
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Q00799;
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     Query Match
Best Local S
Matches 84
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RBP2_PLAVB
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Length 1251;

Score 129; DB 1; Pred. No. 5.9;

6.5%;

Query Match Best Local Similarity

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732 VGIKITPELALTELLGDAKLKTAQELKFESKNNVVLETENMSKNTNELDVHKNIQDAYKV 791
                                                                                                                                       LEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQ 126
                                                                                                                                                                                                                                                                                      -----VDLYNKASSLITKTLDPLNGGTLLDSNEIT--TANKN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                  INNTLSTINEQKTNADALSNSF - - - IKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FINLESVKHNLSEITNIK------QGGEKI-----YSKAKDIMQKIKATSENTAEKT 469
                                                                                                                                                                                                    LEKVKDDQSNYVNYLNQITTER-----NLIVTEKNRLNGIDSTITNIEG----ALKE 517
QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE-----TVNNNLNAT 66
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MEDLINE-95219088; PubMed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
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STRAIN=168 / BGSC1Al;
BADLINE-97124196; Pubmed-8969509;
YOShida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N., Miwa Y., Fujita Y.;
                                                                                                                                                                                                                                                                                                                                                       518 SKGNYEIGFLEKLEEIGKNRKLKVDITKKS---INSTVG--NFSSLFNNFDLNQYDFNKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // Ain a fit 
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01-MAR-2002 (Rel. 41, Last annotat
Wall-associated protein precursor.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
containing the lic and cel loci, and creation of a 177 kb contig
covering the gat-sacxy region.";
Microbiology 142:3113-3123(1996).
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
MOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
INTO THE MEDIUM.
                                                                                                                         SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                          -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
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                                                                                       101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.
                                                                                                                                                                                                                                                                                                                                                                                   3 X 101 AA APPROXIMATE TANDEM REPEATS.
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1-3.
31 X 21 AA APPROXIMATE TANDEM REP
X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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1 28 OR 32 (POTENTIAL).
29 2334 WALL-ASSOCIATED PROTEIN.
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EMBL, D31856; BAA0656.1; -.
EMBL, D29985; BAA06560.1; -.
EMBL, D83026; BAA11683.1; -.
EMBL, 299124; CAB15959.1; -.
PIR, S32920; S32920.
Subtilist; BG10797; wapA.
InterPro; IPR003305; CBD_6.
Ffam; PF02018; CBD_6: 1.
Cell wall; Repeat; Signal; Comp
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MEDLINE-92078147; Pubmed-1744083;
Garrison K., Mackrell A.J., Fessler J.H.;
Drosophila laminin A chain sequence, interspecies comparison, and domain structure of a major carboxyl portion.";
J. Biol. Chem. 266:22899-22904(1991).
-!- FUNCTION: BINDING TO CELES VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
                                                                                                                                                                                                                                                                                                                   1993 TYTWDAEDNLTAVTKKGEDKPFATYKY------DEKGNRIQKTVNGKV-TNYFYDGDS 2043
                                                                                                 1772 SVVNKEQNTTKKRTFDNKNRLTELTDRGGSQTWTYPSDSDKLK---TFSWIHGDOKGTNO 1828
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                                      Gaps
                                                                        3 SITKKDANPNNGQTQLEAARM-ELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN- 60
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"Genetic analysis of laminin A reveals diverse functions during
morphogenesis in Drosophila.";
                                                                                                                                               61 ---NNLNATLEQLKMAKT-----NLESAINQANTDKTTFDNEHPNLV-----
                                        113;
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   Length 2334;
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MEDLINE-93049203; PubMed-1425586;
Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,
                                      Indels
   DB 1;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Laminin alpha chain precursor.
LANA OR LANA.
6.4%; Score 128.5; I 22.1%; Pred. No. 14; iive 56; Mismatches
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MEDLINE=94038678; PubMed=8223265;
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EMBO J. 11:4519-4527(1992).
                                      91; Conservative
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                     Similarity
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DOMAIN IN EGF-LIKE 12.
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@ilenseric.
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EMBL; M96388; AAC37178.1; ...

EMBL; M75882; AAA28662.1; ...

EMBL; M75882; AAA28661.1; ...

ENBL; M75882; AAA28661.1; ...

ELYBase: FB90000226; LanA.

InterPro: IPR000034; Laminin_B.

InterPro: IPR00134; Laminin_B.

InterPro: IPR00134; Laminin_B.

InterPro: IPR00130; Premyltin.

Ffam; PF00052; laminin_B; 1.

Ffam; PF00053; laminin_B; 1.

Ffam; PF00053; laminin_B; 1.

Ffam; PF00053; laminin_Cfc; 20.

Ffam; PF00033; Laminin_B; 1.

Frobom; PF00031; Laminin_B; 1.

Frobom; PF00031; Laminin_B; 1.

Frobom; PF00031; Laminin_B; 1.

Frobom; PF00032; Lamin; 1.

FROSTTE; PS01186; EGF_1; 17.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS00025; LAMININ_TYPE_EGF; 19.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_1; 17.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_1; 17.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_1; 17.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; PS01186; EGF_2; 5.

FROSTTE; FS00126; EAMININ_TYPE_EGF; 19.

FROSTTE; FS00126; EAMININ_TYPE_EGF; 19.

FROSTTE; FS00126; EAMININ_TYPE_EGF; 19.

FROSTTE; FS00126; EAMININ_TYPE_EGF; 19.

FROSTER: FS00126; EAMININ_TYPE_EGF; 19.

FROSTER
       CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
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LAMININ N-TERMINAL (DOMAIN VI).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5.
LAMININ EGF-LIKE 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNAD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSLSKSKKGEVTFSPYSNSGAFSF-----SNAI-----LNGGSVSGLQRRDDTE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 GSVNNGEIN-------LDNGSTYVIVEPVSGKGTVNIS---GNLYLHYP 496
                                                                                                                                                                                                                                                                                                                                                                                                                           SVSQSSSSASDVSSSVSQSSSSASDVSSSVSQSASSASD-----VSSSVSQSASSTSD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 ATASNSLSSSDGTIYLPTTTISGDLTLTGKVIATEGVVVAAGAKLTLLDGDKYSFSADLK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 VYGDLLVKKSKETYPGTEFDISGENFDVTGN--FNAEESAATSASIYSFTPSSFDNSGDI 411
                                                                                                                                                                                                                                                                                                                                         6.4%; Score 128; DB 1; Length 995;
llarity 16.1%; Pred. No. 5;
Conservative 100; Mismatches 152; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   SITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSQSVSS----ASGSSSSFPQST----SSASTASGSATSNSLSSITSSASSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ALSNSFIKK-----VIQNNEQSF---VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 TFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE---PSSRILANTNSITDVSWIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLA-GTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATST-
                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN YIL169C.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

F635287A038137EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 106.1 kDa protein in GLY1-GDA1 intergenic region.
  Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956 AA
                                                                                                                                        EMBL; 246921; canc...
SGD; S0001431; YIL169C.
InterPro; IPR004089; Chemotaxis_transducer.
InterPro; IPR000727; T_SNARE.
InterPro; inrotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497 DIFIGOIVVFKGEGVLAVDPIEINATPIPVVGY 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SSNENNADKIP--GY
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35
468
664
99735 MW;
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28 35
468 4
664 6
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Best Local Simi
Matches 73;
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P32618;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNGP-----ERITSDKYVADGRWYQAVVDRMGPNAKLTIREELPNGD-----VVVEHS 2792
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                                                                                                                                                                                                                                                                                                                                                                       ANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIR-----NNLVDLYNKA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 ANNTTANPTPAVDEIKVAKIVLSGL-----RFGQN---TIELSVPTGEGNMNKVAPMI 368
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                               TDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQ-- 83
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STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----BNLKAQVEAARQLANSIKV-GVNFK-------PSTILELKTPEKT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 YSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                       Length 3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAX-2000 (Rel. 39, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region precursor.
YIL169C OR Y19402.07C.
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                      ; Score 128.5; DB 1;
; Pred. No. 24;
48; Mismatches 155;
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  6.48;
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YIQ9_YEAST
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01-MAR-2002
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Q12355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETVNNNLN-ATLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 ---SNSFIKKVIQNNE-QSFVGTFTNAN----VQPSNYSFVA-----FSADVTPVNYK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561 IQPSSSLLSQLTQDTDNRSMLSNHISSNNENKQQPSSYSHALPTTATANATATATN-G 619
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                                                                                                     Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avilligan J.T., Tennessey K.M., Allen E., Araujo R., Avilles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petell F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 Bateman A., Chothia C.; "Fibronectin type III domains in yeast detected by a hidden Markov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ITKKDANPNNGQTQLEAARMELTDL-----INA-KAMTLASLQDYAKIEASLSSAYSEA
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                                       Komp
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SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-III.
                                     Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., F
Wel Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                          FIBRONECTIN TYPE III DOMAIN.
MEDLINE-97148176; Pubmed-8994808;
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InterPro; IPR003961; FN_III.
Pfam: PF00041; fn3, 1.
SWART; SW00060; FN3; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U18779; AAB64999.1;
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                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=4932;
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Terachina H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terachina H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
"Up-regulation of genes encoding glycosylphosphatidylinositol
(GPI) attached proteins in response to cell wall damage caused by
disruption of FKS1 in Saccharomyces cerevisiae.";
Mol. Gen. Genet. 264:64-74(2000)
--- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR AND
SECRETED BY REGENERATING PROTOPLASTS.
--- SIMILARITY: BELONGS TO THE SPS2 FAMILY.
                                                                           678 KGFTTDELDNYWTKQQPQVRSTNESLFSTTGTPMSSYK-----ANPVISPY--SSSHLR 729
                                                                                                                                                      --GONTIELS-- 353
                                                                                                                                                                                                                      730 QTSNATNINPMHPQSLLAATLNDPSLQSFVRSGSFYSAPQPANSLQNNINGNETENISPR 789
--PSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-96381250; PubMed-8789263;
Brandt P., Ramlow S., Otto B., Bloecker H.;
"Nuclocide sequence analysis of a 32,500 bp region of the right arm
of Saccharomyces cerevisiae chromosome IV.";
Yeast 12:85-90(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pardo M., Monteoliva L., Pla J., Sanchez M., Gil C., Nombela C., "Two-dimensional analysis of proteins secreted by Saccharomyces cerevisiae regenerating protoplasts: a novel approach to study the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 -----VPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                         790 ISSDFNLLVPNLSPRISNDVPIVPCNNTTLTPSHSNILTMHQPTADNI 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                      QVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRF---
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SIGNAL 1 19 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protoplast secreted protein 1 precursor.
PST1 OR YDR055W OR D4214 OR YD9609.09.
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MEDLINE=99251092; Pubmed=10234784;
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COMPLUYEAST-2DPAGE; Q12355;
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                                                                                                                                                               PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDa, 42 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 150
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                                                                                  Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 KVIQNNEQSFVGTFTNANVQPSNYSFV-----AFSADVTPVNYKYARRTVWNGDEPS
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Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN REPEAT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GG----TLLDSN-EITTANKNINNTLSTINEOKTNADAL----
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MEROZOITE
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InterPro; IPR000561; EGF-like.
                                                                 REVISIONS, SEQUENCE FROM N.A.
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TSFAADSLESITDSLNLQSLTILT------SASFGSLQSVDSIKLITLPAISSFT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|::|| | :| : | : | : || SNIKSANNIYISDTSL-----QSVDGFSALKKVNVFNVNNKKLTSIKSPVETVSDSLQ 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVKLSSTSKSQSS-----QTTAKVSKSSSKAEEKKFTSGDIKAAASASSVSSGGSS-- 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS--TAYNQIRNNLV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLYNKASSLITKTLDPL----NGGTLLDSNEITTANKN-----INNTLSTINEOKTNA 181
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3%; Score 126.5; DB 1; Length 444; 18.1%; Pred. No. 2.3;
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230F60CACA5921A4 CRC64;
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444 AA;
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CRC64;

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--SNSFIK 190

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                                                                                                                                                                                                                                                                                                                                                                                         Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                 13.AUG-1987 (Rel. 05, Created)
01-FRB-1996 (Rel. 33, Last sequence update)
01-FRB-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
327 TPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 382
                     (POTENTIAL).
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InterPro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
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Gaps

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Length 1639;

6.3%; Score 126.5; DB 1; 20.7%; Pred. No. 11; tive 62; Mismatches 155;

Conservative

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                                                                                                                    151 GG----TLLDSN-EITTANKNINNTLSTINEQKTNADAL------SNSFIK 190
                                                                                                                                    333 SGNTPNTLLDKNKKIEEHEKEIKEIAKTI---KFNIDSLETDPLELEYYLREKNKNIDIS 389
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               LASLQDYAK----IEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTT 90
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copyr ein - protein se June 1 June 1 score: 1998 e: 1 CMS1 table: BLOSUM d: 562222 umber of hits sa	Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 100% Listing first 45 summaries Database: SPTREMBL_19:* 1: sp_archea:* 2: sp_archea:* 3: sp_fungi:* 4: sp_hunan:* 5: sp_hunan:* 5: sp_hunan:* 6: sp_ivertehivate:*	6: Sp_mammal:* 7: Sp_mammal:* 8: Sp_organale:** 9: Sp_porganale:* 10: Sp_plant:* 11: Sp_rodent:** 13: Sp_vertebrate:* 14: Sp_vertebrate:* 15: Sp_vertebrate:* 16: Sp_bacteriap:* 17: Sp_archeap:* 17: Sp_archeap:* 17: Sp_archeap:* 17: Sp_archeap:* 18: Sp_archeap:* 19: Sp_archeap:* 10: Sp_archeap:* 10: Sp_archeap:* 17: Sp_archeap:* 18: Sp_archeap:* 19: Sp_archeap:* 10: Sp_archeap:* 10: Sp_archeap:* 10: Sp_archeap:* 11: Sp_archeap:* 12: Sp_archeap:* 13: Sp_archeap:* 14: Sp_archeap:* 15: Sp_archeap:* 16: Sp_archeap:* 16: Sp_archeap:* 17: Sp_archeap:* 18: Sp_archeap:* 18: Sp_archeap:* 19: Sp_archeap:* 19: Sp_archeap:* 10: Sp_archeap:* 11: Sp_archeap:* 12: Sp_archeap:* 13: Sp_archeap:* 14: Sp_archeap:* 15: Sp_archeap:* 16: Sp_archeap:* 16: Sp_archeap:* 17: Sp_archeap:* 18: Sp_archeap:* 18: Sp_archeap:* 18: Sp_archeap:* 19: Sp_archeap:* 10: Sp_archeap:*	Score Match Length DB 1200 131.5 41.9 671 2 131.5 41.9 671 2 131.5 41.9 671 2 131.5 41.9 671 2 131.5 41.9 671 2 144 37.7 702 2 144 37.2 649 2 143 37.3 644 2 143 37.3 644 2 143 37.3 644 2 143 37.2 649 2 13 35.7 647 2 13 35.7 647 2 13 35.7 647 2 13 35.7 647 2 13 35.7 647 2 10 35.2 656 2 10 5 31.0 419 2 15 5 28.8 386 2

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                                181 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                           40;
                                                                                                                                                                                                                                                                                      Pharm G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D., May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of Mycoplasma gallisepticum.";
Submitted (DEC-199) to the EMBL/GenBank/DDBJ databases.
EMBL, AF210770, AAF29524.1;
SEQUENCE 671 AA; 71898 MW; 4D6AE6B59175D679 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.2.
Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                   Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                         75; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.4%; Pred. No. 1.1e-33;
Matches 179; Conservative 75; Mismatches 118
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                                                                                                                                                                                                                                      Mycoplasmataceae; Mycoplasma
NCBL_TaxID=2096;
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                                                                             241 PSSRI 245
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267 PSSRI 271
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STRAIN=S6;
MEDLINE=95010739; PubMed=7925999;
MEDLINE=95010739; Clew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browtham F.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browthing G.F., Whithear K.G., Walker I.D.;
"The organisation of the multigene family which encodes the major cell
surface protein, pMGA, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
EMBL: L28424; AAA62418.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 AADANNVGLQYKLNNGNVQQVEFATS-----TSANN-----TTANPTPAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHFATIKTNLTALYQSGKDIVTKTLDPLM-GTAINLSAVSQANTNISNAVSKLETWKTNA
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NCBI_TaxID=29560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.6%; Score 831.5; DB 2; Length 702;
42.0%; Pred. No. 2.1e-33;
tive 84; Mismatches 116; Indels 39.
                                                                                           Wycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 EIKVAKIVLSGLREGQNTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK
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B70AC874FE85055C CRC64;
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Last sequence update)
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Last annotation update)
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75517 MW;
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                                                                                                                Bacteria; Firmicutes; Bacill
Mycoplasmataceae; Mycoplasma
01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PMGA1.4 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.69
Best Local Similarity 42.09
Matches 173; Conservative
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                                                                                                                                                    NCBI_TaxID=2096;
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Gaps

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69 NPNSGNTTPEQQLAAARKTLTDLLGTENTNVALYADYAKIQSTLSTAYMTAKTASENTSA 128
                                                                                                                                                                                      TLEOLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEORATNLEGLSSTAYN 125
                                                                                                                                                                                                                126 QIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALS 185
                                                                                                                                                                                                                                                                                                                                                                                         235 VWNGD----EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKA 291
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                                                                                              10 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA 65
                                                                                                                                                                                                                                                                                                   186 NSFIKKVIQNNEQSFVGTFTNAN--VQPSNYSFVAFSADVTP-----VNYKYARRT
                                                     60;
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STRAIN-HS;
STRAIN-HS;
Shen O.C., Bi D.R., Weng C.J.;
Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS ";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF991414.1; -.
SEQUENCE 680 AA; 72909 MW; A2ABC6500E3DFE47 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
      Length 584;
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         40.3%; Score 805; DB 2; Length 58.
42.4%; Pred. No. 3.4e-32;
iive 72; Mismatches 113; Indels
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Last annotation update)
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      Query Match
Best Local Similarity 42.44
Matches 180; Conservative
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Matches 164; Conservative
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Best Local Similarity
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MEDLINE-99392472; PubMed-10463176;
Markham P.F., Duffy M.F., Glew M.D., Browning G.F.;
"A gene family in Mycoplasma imitans closely related to the pMGA family of Mycoplasma gallisepticum.";
Microbiology 145:2095-2103(1999).
EMBL; AF141940; AAD39483.1; -.
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"Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91415.1; -.
InterPro; IPR001986; EPSP_syntase.
PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID-2096;
                                                                                                                                                                                                                                                                                                   Length 632;
                                                                                                                                                                                                                                                                                                 Query Match 41.3%; Score 826; DB 2; Length 63
Best Local Similarity 45.3%; Pred. No. 3.4e-33;
Matches 183; Conservative 65; Mismatches 120; Indels
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Last annotation update)
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SIGNAL
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LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDEIKVA 336
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                                                                                                      8 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                     44 DINPGDGGGMMNAASQELAAARMGLTTVFDSRAKNLGLYVDYKKTQDFLTKAYDAAKTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 DNSSSTTQNLNEAKTRLETAIRTAATSKQTFDEQHAELVKVYEELKTTLSNETATLAPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 INADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV------NYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PG31, ATCC19610;
MEDLINE-99003182: PubMed-9784576;
Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.;
Liu L., Payne D.M.
A protein (M9) associated with monoclonal antibody-mediated
agglutination of Mycoplasma gallisepticum is a member of the pMGA
                                                                                 NTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmatacee; Mycoplasma, NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 645;
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Infect. Immun. 66:5570-5575(1998).
EMBL; AF032890; AAC69269.1; -. SA2F29572CFAE055 CRC64;
SEQUENCE 645 AA; 69876 MW; SA2F29572CFAE055 CRC64;
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Last annotation update)
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Best Local Similarity 42.3%; Pred. No. 2.9e-29;
Matches 172; Conservative 64; Mismatches 123
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ANNVGLQYKLNNGNVQQVEF - - - -
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(TrEMBLrel. 10, I
(TrEMBLrel. 10, I
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01-MAY-1999 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP-----VNYKYARRTVW 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGD--EPSSRILANTN-SITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAAD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIRNNLVDLYNKASSLITKTLDPLNG--GTLLDSNEITTANKNINNTLS--TINEQKTNA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
                                                                                                                                                                                                                                     TVWTADSRTWTSPLPNNLQNSAPLTDVSWIYTLSGTGAKYTLTFDYYGPQTGYLYFPYKL 353
                                                                                                                                                                                                                                                                                                                                  411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKAADANNVGLQYKLNNGNVQQVEF--------ATSTSANNTTANPTPAV
                                                                                                                                                                                                                                                                                                                         || :| ||||||||| : ::|
VKTSD--KVGLQYKLNQADPVAIQFSEAAATASAPAĒTDGRQESAĒTĀTĀNĒKVNPMPSV
                            TVWNGD-----EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKL
                                                                                                  INEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 702;
           121 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL---
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273E8915FEE57B9F CRC64;
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Last annotation update)
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41.6%; Pred. No. 1.3e-29;
tive 62; Mismatches 127
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75537 MW;
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Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 QYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTAGAVTMANTKIVEAIKDEVLNPKKEN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 FPYKLVNTSDQMKLGLEYKLNDA----TEPSAITFGNEQTMNGKTPTVNDINVAKVTLAN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 NPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN 62
                  MEDLINE-95010739; PubMed-7925999;
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Browning G.F., Whithear K.G., Walker I.D.,
The organisation of the multigene family which encodes the major
surface protein, pMGA, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIVW-NGDEPSSRILANT----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLY
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|RIIFTNGDEP--RSVSNTPVDGQTMAQPLSNVSWIYSLAGTGAKYTLEFTYYGPSTGYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 FPYKLVKAADANNVGLQYKLNNGNVQOVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                           Markham P.F.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                      HAEMAGGLUTININ.
3ABACDB65940EBBB CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                             37.2%; Score 744; DB 2; Le
42.9%; Pred. No. 3.7e-29;
ive 62; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 LRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI
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                                                                                                                                                                                                                                                                                                               25 PC
650 HA
70249 MW;
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NCBI_TaxID=2096;
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                                                                                                                                                                                                                                                                       EMBL; U90714; AAB50152.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.9
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum.
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26 6
650 AA;
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01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||||| :| :||:||||
LXFPYKLVNTSDQVKLGLEYKLND------ATKPSAITFGSEQTMNGKTPTVNDINVA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                  Liu L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.; A protein (M9) associated with monocional antibody-mediated agglutination of Mycoplasma gallisepticum is a member of the pMGA family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNADALSNSF1KKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARRIVW-NGDEPSSRILANT----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                   Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ll protein.
644 AA; 69866 MW; 8B9F352B13FBDE5C CRC64;
                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 69.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.3%; Score 745; DB 2; 42.3%; Pred. No. 3.3e-29;
                       644 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 66:5570-5575(1998).
EMBL; AF053978; AAC69274.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-PG31, ATCC19610;
MEDLINE-99003182; Pubmed-9784576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                 Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
HAEMAGGLUTININ PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum.
                     PRELIMINARY;
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SEQUENCE FROM N.A.
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                                          O9ZHR9
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                     Q9ZHR9
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Q49495
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Q9ZHR9
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NYKYARRTVWNGDEPSSRILANTNS-----ITDVSWIYSLAGINTKYQFSFSNYGPS 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 ENATKLADSLLSSIVKKITGVEE-----AHNKAQPANYSFVGYKRWYTELLLDKQVFP 279
                                                                                                                                                                                                                                                                                               STGYLYFPYKLVKAADANNVGLQYKLNNGNVQOVEFATSTSA----NNTTANPTPAVDE 332
                                                                                                                                                                                                                                                                                                                  63 DINPGGGQNMMDSAAQELTAARTALTSLLASKNANVEWYSDYAKIQNTLIAAYTTAEQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNADALSN--SFI--KKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----
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                                                                                                                               NYKYARRTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
                                                                                                                                                                                                                                                           NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS
                                                                 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
                                                                                                                                                                       TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the pMGA multigene family of Mycoplasma "Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91413.1; -
SEQUENCE 656 AA; 70875 MW; 58EA7E075FC617E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                             IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI
                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 35.2%; Score 704; DB 2; Local Similarity 41.0%; Pred. No. 3.4e-27; les 166; Conservative 67; Mismatches 124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 LYFPYKLVNTSDQVKLGLEYKLND-----ATKPSALTFGSDQTMNGKTPTVNDINVA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                          STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 178
                                                                                                                                                                                                                                                                                                                              NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 120
                                                                                                                                                                                                                                                                 pMGA,
                                                                                                                                                                                     DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA-----NNTTANPTPAVDEIKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                   ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93162830; PubMed-8432610;
MARKham P.F., Glew M.D., Whithear K.G., Walker I.D.;
MAlecular clothing of a member of the gene family that encodes lemagglutinin of Mycoplasma gallisepticum.";
Infect. Immun. 61:903-909(1993).
EMBL; M83178; AAA029651; -.
EMBL; S55216; AAB25397.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  647;
                                                                                                                          Length 649;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 713; DB 2; Length 41.1%; Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEMAGGLUTININ HOMOLOG.
33916673BB9E28C4 CRC64;
                                                               POTENTIAL.
356554BD2C72C1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                       Query Match 37.2%; Score 743; DB 2; I
Best Local Similarity 42.3%; Pred. No. 4.1e-29;
Matches 172; Conservative 62; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacilla
Mycoplasmataceae; Mycoplasma
NCBL_TaxID=2096;
                                                                 25
70205 MW;
                FEBS Lett. 352:347-352(1994).
EMBL; L28424; AAA62416.1; -.
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VRLTGLAFGKNT 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 GTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; The organisation of the multigene family which encodes the major surface protein, pMGA, of Mycoplasma gallisepticum."; FEBS Lett. 352:347-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 AMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFD
                                                                           TGYLYFPYKLVKAADANNVGLQYKLN-NGNVQQVEFATSTSANNTTANPTPAVDEIKVAK
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Markham P.F.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; U90714; AAB50154.1; -

InterPro; IPR002819; HD.

CONTENTE 703 AA; 75742 MW; 310B69BE9F73CBC5 CRC64;
                                                                                                                                                                                                                 338 IVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 382
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Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DPKYSAILDQINGVSCKGEELVQHTLDPVS-GIVPAANTITEEITKIEEVISEKTLQDQK
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323 TANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=F;
Pharr G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D.,
May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 419;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210770; AAF29525.1; -.
NON.TER 419 419
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.3 (FRAGMENT).
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Scoring table: Sequence:

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Chimeric; Marek's disease virus; outer membrane protein; fusion protein; antigen; vaccine; poultry.
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- Mycoplasma gallisepticum.
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M.gallisepticum 26
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1 GCMSITKKDANPNNGQTQLE......SSNENNADKIPGYRRPGTFL
                                                                                                                                                June 12, 2002, 10:48:38; Search time 55.68 Seconds
                                          Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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AAP05081
AAR79911
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Score

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Staphylococcus aur Staphylococcus aur ż

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This sequence represents the chimeric protein 40 K-C which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antiqenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
                                                                                                                                                                                                                                 Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                            Disclosure; Page 22-30; 51pp; Japanese.
                                                                                                                                                             Yanagida
                                                                     97WO-JP01084
                                                                                                  96JP-0103548
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                                                                                                                                                            Tsuzaki Y,
                                                                                                                                                                                         WPI; 1997-503046/46.
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                                                                                                                                                                                                       N-PSDB; AAT96596
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                                                                                                                             This sequence represents the chimeric protein 40 K-S which comprises a fragment of the Marek's disease virus outer membrane protein gB fused to an antigenic protein from Mycoplasma gallisepticum. The chimeric protein can be used in recombinant live vaccines for prevention of infection by Mycoplasma gallisepticum, especially as the outer membrane protein shows antigenicity in poultry.
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/note= "derived from Marek's disease virus gB protein"
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                                           Fusion protein comprising herpes virus outer membrane protein and antigenic polypeptide – for prevention of infection by Mycoplasma
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/note= "derived from M. gallisepticum antigen"
                                                                                                                                                                                                                                                                                 Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid Marek's disease virus/M. gallisepticum 40 K-C protein.
                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                              Score 2004; DB 18;
Pred. No. 1.3e-128;
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    Marek's disease gammaherpesvirus.
    Mycoplasma gallisepticum.

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                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 16-19; 51pp; Japanese
                                                                     gallisepticum, especially in poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36051 standard; Protein; 1086 AA
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 394; Conservative
WPI; 1997-503046/46.
N-PSDB; AAT96595.
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                                                                                                                                                                                                                                      456 AA;
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Chimeric
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                                                                                                                                          EPSSRILLANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGL
                                                               1 GCMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV
                                                                                                                                                                                        SSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKT
                                                                                                                                                                                                                                                      NADALSNSFIKKVIQNNEQSFVGTFINANVQPSNYSFVAFSADVTPVNYKYARRTVWNGD
                                                                                                                                                                                                                                                                                                                                      OYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEG
   Length 1086;
Score 2000; DB 18;
Pred. No. 7.5e-128;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NMNKVAPMIGNIYLSSNENNADKIPGYRRPGTFL 394
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 99.88;
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387 mnkvapmigniylssnennadki 409
                                                                      AAR63229;
                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                                                                                                                     A restriction fragment of the insert of M.gallisepticum genomic clone pUM-67 containing an open reading frame was sequenced (AAQ77857). The ORF encodes an antigenic polypeptide (AAR63230). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                        Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                 TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 615;
                    recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                              Ohsawa I;
                                                                     1.615
/note= "Trp residues correspond to
                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.3%; Score 1910; DB 15; 98.2%; Pred. No. 4.7e-122; ive 3; Mismatches 4;
                                                                                                                                                                                                                               ŝ
Mycoplasma gallisepticum antigen (UM-67).
                                                                                                                                                                                                                               Ohkawa
                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 87-91; 123pp; Japanese.
                                                            Location/Qualifiers
                                                                                                                                                                                                                               Iritani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                       Funato H, Irrum.
                                                                                                                                                                93JP-0074139.
93JP-0245625.
                                                                                                                                             94WO-JP00541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                      gallisepticum
                                                                                                                                                                                                                                                            WPI; 1994-333181/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 376; Conserv
                                                                                                                                                                                                                                        Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                     615 AA;
                                                                                                                                                                                                                                                                                                               of a live vaccine
                                                                                                                                                                                                                                                                       N-PSDB; AAQ77857.
                                                                                                                                             31-MAR-1994;
                                                                                                                                                                31-MAR-1993;
                                                                                                    WO9423019-A
                                                                                                                        13-OCT-1994
                                         Mycoplasma
                                                                                                                                                                                                                               ś
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                         Saeki S,
                                                                      Protein
                                                                                                                                                                                                                               Аоуата
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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A restriction fragment of the insert of M.gallisepticum genomic clone pUM-66 containing an open reading frame was sequenced (AAQ77856). The ORF encodes an antigenic polypeptide (AAAR3229). A recombinant avipox virus comprising the coding sequence can be used as a live vaccine to protect against infection by Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 cmsitkkdanpnngqtqleaarmeltdlinakamtlaslqdyakieaslssayseaetvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 610;
                                                                                                                                                                        recombinant avipox virus; live vaccine; mycoplasma antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohsawa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 1856; DB 15;
95.5%; Pred. No. 2.2e-118;
iive 10; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohkawa
                                                                                                                              Mycoplasma gallisepticum antigen (UM-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 78-81; 123pp; Japanese.
                                                                                                                                                                                                                                                        Location/Qualifiers
  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H, Iritani Y,
Takahashi K;
AAR63229 standard; Protein; 610
                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-JP00541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0074139
93JP-0245625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.5%;
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LID.
                                                                                    (first entry)
                                                                                                                                                                                                                Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Funato H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-333181/41.
N-PSDB; AAQ77856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1993;
30-SEP-1993;
                                                                                    23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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nnlnatleglkmaktnlesainqantdkttfdnehpnlveaykalkttlegratnlegla 146
                                                                                                                                                          PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The plasmid pUTTW-IP contains a sequence (the TTW-I gene) coding for the 40kD antigen of Mycoplasma gallisepticum under the control of a synthetic promoter. A 1300 bp restriction fragment containing the promoter-ORF sequence was excised and was used in the construction of plasmid pNZ7929-R2. This in turn was involved in the construction of a recombinant aviox virus vector comprising the TTW-I gene, DNA encoding the signal membrane anchor peptide from Newcastle Disease Virus heemagglutinin neuraminidase and FPV sequences. The recombinant avipox virus is useful as a live vaccine
                             STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant avipox virus combining DNA encoding a polypeptide exhibiting antigenicity of mycoplasma, useful for the production of a live vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant avipox virus; live vaccine; mycoplasma 40kD antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohsawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "corresponds to a NNN codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "corresponds to a NNN codon"
                                                                                                                                                                                                                                               302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gallisepticum 40kD antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 71-74; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        AAR63227 standard; Protein; 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-JP00541
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93JP-0245625
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma gallisepticum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-333181/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saitos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ77854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                           AAR63227;
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                                    27 cmsitkkdanpnngqtqlqaarmeltdlinakartlaslqdyakieaslssayseaetvn 86
                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN~61
                                                                                    YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence coding for the 40kDa antigen was obtained by PCR amplification of M.gallisepticum genomic DNA. The antigen reacts with Mycoplasma-immune or Mycoplasma-infected serum and can be used as a vaccine to protect fowl from M.gallisepticum infection.
                       PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "corresponds to NNN codon in AAQ53419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "corresponds to NNN codon in AAQ53419"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum antigen and DNA coding for it for vaccination of fowl against mycoplasma infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.4%; Score 1612; DB 14; 95.0%; Pred. No. 4.8e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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6; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohkawa S,
                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; mycoplasma infection; poultry; fowl.
                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum 40kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 23-26; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aoyama S, Fujisawa A, Iritani Y,
                                                                                                                                                                                                                                                                   Ä.
                                                                                                                                                                        AAR44493 standard; Protein; 368
                                                                                                                                                     MNKVAPMIGNIYLSSNENNADK 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92JP-0138819
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                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma galliseptícum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-405837/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 320; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ53419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                             AAQ94711 encodes AAR76955 Mycoplasma gallisepticum antigenic protein TTM-1. TTM-1 can be used as a vaccine for M. gallisepticum infectious diseases in poultry, and as a diagnostic agent for M. gallisepticum.
                                                                                                                                Gaps
                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This amino acid sequence of MG1 is encoded by M1 DNA and elicits an
                                                                                                                                                                                                                                                                                                                          STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                                                                                                                                                         ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
                                                                                                                                                                                                                                                                                                                                                                 PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Mycoplasma gallisepticum (MG1) polypeptide.
                                                                                                                                                        2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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                                                                                                     Length 368;
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                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antigenic proteins of Mycoplasma gallisepticum
                                                                                                     Score 1604; DB 16;
Pred. No. 1.7e-101;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                  302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma gallisepticum; Poultry vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (JAPG ) NIPPON ZEON KK.
(SHIO ) SHIONOGI SEIYAKU KABUSHIKI KAISHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig.1a; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanagida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                     80.0%;
llarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP93646 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kodama K, Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-358393/49
                                                                                                                    Best Local Similarity
Matches 318; Conser
                                                                  368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN92568
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                                                                    Sequence
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                        182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                                                                                                                                                                                                                                                                                                                          PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                                                                                     NNINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                            Gaps
                                                                                                                                 2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new antigenic protein which reacts with Mycoplasma gallisepticum is useful in a component vaccine for use against poultry infected with M. gallisepticum.
                                                                                                                                                                                                                                                                                      ;
0
                                                                 Length 368;
  to protect against infection by Mycoplasma gallisepticum
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poultry; diagnosis; TTM-1.
                                                                  2; DB 15;
4.8e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma gallisepticum antigenic protein TTM-1.
                                                                                                                                                                                                                                                                                                                                                                                            YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                  Score 1612; D
Pred. No. 4.8e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "any amino acid"
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262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR76955 standard; Protein; 368 AA
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                                                                 Query Match 80.4%;
Best Local Similarity 95.0%;
Matches 320; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigenic protein; vaccine;
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                              368 AA;
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                             Sequence
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NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN
                                                                                                                                   ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
                                                                                                                                                                                       89JP-0136343.
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N-PSDB; AAQ04687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA;
                                                                                                                                                                                                                                                                                                                                                   TMG-1 antigen
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antigen-antibody reaction with anti-MG poultry sera. It can be used as a vaccine to prevent and diagnose MG infection. Doseage is at least 1 micro gram vaccine / kg. No acute toxicity was noted with a dose of 5 mg / kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal
                                                                                                                                                                                                                                                                        62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                                                                                                                                  STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                       Gaps
                                                                                                                                                              61
                                                                                                                                                 2 CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                           182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
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0
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                                                                                            Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 235;
                                                                                                                     Indels
                                                                                           57.0%; Score 1142; DB 10;
.larity 97.0%; Pred. No. 2.8e-70;
Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1142; DB 11;
Pred. No. 2.8e-70;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma gallisepticum; poultry; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial enzyme sequence.
See also AAR05081-2 and AAR06437-41.
                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           incorporated with its coding gene.
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                                                                                                                                                                                                                                                                                                                                                                                                        AAR05081 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.0%;
97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-169109/22.
N-PSDB; AAQ04686.
                                                                                                       Best Local Similarity
Matches 228; Conserv
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                                                     Sequence
                                                                                             Query Match
                                                                                                                                                                                                                                                         122
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DNA encoding the protein can be inserted into an expression vector for the prodn. of MG-1 polypeptide which elicits an antigen-antibody reaction with anti-mycoplasma gallisepticum poultry sera. It may also be ligated to other DNA to produce fusion proteins with an N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnostic and vaccine for poultry mycoplasma serum - utilises antigen protein of the disease and recombinant vector incorporated with its coding gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 261;
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Pred. No. 3.2e-70;
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                                                                                                                                                                                                                             Mycoplasma gallisepticum; poultry; vaccine.
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See also AAR05081 and AAR06437-41.
AAR05082 standard; protein; 261
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97.0%;
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Indels

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AAR79911

AAR79911

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This AA sequence of TWG-1 is encoded by TW-1 base sequence. It has the same sequence as that of a polypeptide expressed in Mycoplasma agalisepticum in nature. When the corresponding DNA sequence is Inserted into a recombinant vector used to transform a host the antigen protein produced can be used as a vaccine to prevent and diagnose MG infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigenic proteins of Mycoplasma gallisepticum – useful as poultry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINE-QKT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JAPG ) NIPPON ZEON KK; (SHIO) SHIONOGI SEIYAKU KABUSHIKI KAISHA
 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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Pred. No. 1.6e-68;
3; Mismatches 4
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                                                                                                                                                                                                                                                                    Mycoplasma gallisepticum; Poultry vaccine; ss;
                                                                                                                                                                                                                                 Amino acid (AA) sequence of TMG-1 polypeptide.
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                                                                                                                        AAP93959 standard; protein; 261
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96.28;
                                                                                                                                                                                                                                                                                                                                                                                                               89EP-0005441.
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                                                                                                                                                                                                (first entry)
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Matches 227; Conservative
                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-358393/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                             AAP93959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of a 261 amino acid protein encoded by a fragment of the Mycoplasma gallisepticum genome. The encoding sequence and the sequence of AAT04075 (encoding a 661 amino acid protein) can be used to detect M.gallisepticum using probes based on nucleotides 1125-1648 and primers based on nucleotides 449-466, the complement of bases 893-919, 1908-1934 and the complement of bases 2184-2210 of AAT04075 and a probe based on nucleotides 718-41 of the DNA encoding this protein. The method using these sequences is faster i.e. is able to detect M.gallisepticum, which causes avian chronic respiratory diseases, within one day, from avian secretions, washings from the lung, respiratory tract, nasal cavity, etc.
                  206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
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                                                                                                                                                                                                                                                                                                                  Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARTV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of Mycoplasma gallisepticum - for the quick detection, i.e. within one day, of avian chronic respiratory diseases
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Pred. No. 3.2e-70;
3; Mismatches 4,
                                                                                                                                                                                                                                                                                   M.gallisepticum 261 amino acid protein.
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                                                                                                                                                                             AA.
                                                                                                                                                                           standard; Protein; 261
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                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma gallisepticum
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N-PSDB; AAT04076.
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Query Match Best Local

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Matches 185; Conservative
                                                          -----ADKIPGY 387
                                                                           456 ptavtvdllkgy 467
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N-PSDB; AAT04075.
                                                                                                                                                                                                                                                                      Misc-difference 270
                                                                                                                                                                                                                                                                                                         Misc-difference 581
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                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                        Misc-difference
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                    Recombinant avipox virus combining DNA encoding a polypeptide - exhibiting antigenicity of mycoplasma, useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                             1..661
/note= "Trp residues correspond to TGA codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                         40.2%; Score 806; DB 15; Length 661;
42.8%; Pred. No. 8.8e-47;
Live 62; Mismatches 123; Indels 6
                                                            recombinant avipox virus; live vaccine; mycoplasma antigen.
                                                                                                                                                                                                                                               Ohsawa I;
                                                                                                                                                                                                                                               Iritani Y, Ohkawa S,
                                           gallisepticum antigen (UM-81).
                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 61-65; 123pp; Japanese.
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                        Saitos, Takahashi K;
                                                                                                                                                                         94WO-JP00541
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93JP-0245625
                                                                                                                                                                                                                     (JAPG ) NIPPON ZEON KK. (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.89
Matches 185; Conservative
                            (first entry)
                                                                                Mycoplasma gallisepticum.
                                                                                                                                                                                                                                                 Funato H,
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N-PSDB; AAQ77853.
                                                                                                                                                                                                                                                                                                                                                                                                                  661 AA;
                                                                                                                                                                                                                                                                                                                       of a live vaccine
                                                                                                                                                                           31-MAR-1994;
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30-SEP-1993;
                            23-JUN-1995
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                                               Mycoplasma
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                                                                                                                                                                                                                                                           Saeki S,
          AAR63226;
                                                                                                             Protein
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                          Detection; probe; primer; PCR; amplification; secretion; lung; avian chronic respiratory disease; respiratory tract; nasal cavity.
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341 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS------
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42.8%; Pred. No. 8.8e-47;
tive 62; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.gallisepticum 661 amino acid protein.
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(SHIO ) SHIONOGI & CO LTD.
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multivalent live vaccines, also new probes for detecting Mycoplasma
                          Disclosure; Fig 3; 81pp; English.
        and manipulating its genome
                                                                                                                   647 AA;
                                                                                                                     Sequence
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                                         62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                      341 LSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSS--------NENN 380
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                                                                                                                   ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                                                                                                                                                        -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 294
       DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New promoter region from a Mycoplasma gallisepticum adhesin gene useful when coupled to foreign antigen gene, for prodn. of
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/label- Sig_peptide
/note= "the signal peptide shows homology '
the pMGA1.3 signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                           Adhesin; pMGA; mycoplasma; diagnosis; vaccine; vector; respiratory disease; poultry; haemagglutinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma gallisepticum strain S6.
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93AU-0050593.
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                                                                                                                                                                                                                                                                     381 ----ADKIPGY 387
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456 ptavtvdllkgy 467
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Adhesin pMCA1.2 (AAW11978) and adhesin pMCA1.3 fragment (AAW11979) are products of gene sequences (see also AAF15131) isolated from Mycoplasma gallisepticum. DNA constructs incorporating the promoter and/or signal sequences of the pMCA genes can be used in the prodn. of multivalent live vaccines. The signal peptide sequence is utilised where attachment of an exogenous antigen gene to the mycoplasma cell membrane is required.
                                                                                                                                                                                                                                                                                                                                                                                                                    9 DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 NYKYARRTVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TN----ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV----
                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                         Length 647;
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                                                                                                                                                                                                                                                                                                                                                              124; Indels
                                                                                                                                                                                                                                                                                                         35.6%; Score 713; DB 16; 41.1%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                              60; Mismatches
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Job time: 387 sec
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Best Local Similarity
Matches 169; Conserva
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Appli Appli Appl 4, Appli 4, Appli App]

Sequence Sequence Sequence sequence

Sequence 2 Sequence 2 Sequence 2 Sequence 4 Sequence 4 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 3 Sequence 3

Appli Appli Appli

Sequence

Perfect score:

Title:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB & Maximum DB &

Database

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APPLICANT: Obsawa, Ikuroh
APPLICANT: Funato, Hirono
APPLICANT: Iritani, Voshikazu
APPLICANT: Askanashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND
ADDRESSEE: NAUGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: UP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: UP 05-074139
FILING DATE: 31-MAR-1993
APPLICATION NUMBER: UP 05-074130
FILING DATE: UP 05-074130
FILING DATE: UP 05-074130
FILING DATE: UP 05-074130
FILING DATE: UP 05-074130
                     US-09-268-347-28

US-09-268-347-34

US-08-114-481-2

US-08-114-481-2

PCT-US95-06111-2

US-09-268-347-49

US-09-268-347-49

US-09-347-47

US-08-169-927-2

US-09-336-447A-15

US-08-13-467-4

US-08-13-467-4

US-08-13-336-447A-15

US-09-377-155-33

US-09-977-155-33

US-09-977-155-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: UP 05-245625 FILING DATE: 30-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/JP94/0054 FILING DATE: 31-MAR-1994 ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08525742 Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito, Shuji
Ohkawa, Setsuko
Saeki, Sakiko
746
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APPLICANT: Saito,
                        USA
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STREET: 17:
CITY: Wash.
STATE: DC
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APPLICANT:
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1 GCMSITKKDANPNNGQTQLE.....SSNENNADKIPGYRRPGTFL
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                                                Compugen Ltd
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US-08-525-742-4
US-08-525-742-4
US-08-525-742-2
US-08-523-742-2
US-08-523-992A-8
US-09-541-782-6
US-09-541-782-6
US-09-541-782-6
US-09-541-782-6
US-09-268-347-30
US-09-268-347-30
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US-08-923-992A-4
US-09-268-347-48
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US-09-043-123-2
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US-08-728-470-2
US-08-617-697-2
US-08-719-641-2
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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US-08-530-198-2
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Maximum Match 100%
Listing first 45 summaries
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302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGN 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.6%; Score 1856; DB 2;
95.5%; Pred. No. 3.5e-128;
iive 10; Mismatches 7;
PatentIn Release #1.0, Version #1.30
                               PAPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             PCT/JP94/00541
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08525742
Patent No. 5871742
GENERAL INFORMATION:
APPLICANT: Salto, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 MNKVAPMIGNIYLSSNENNADK 383
                                                                                                                                                                                                                                                                 NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saito, Shuji
Ohkawa, Setsuko
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-8870357
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohsawa, Ikuroh
Funato, Hirono
                                                                                                                                                                                                                              FILING DATE: 31-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saeki, Sakiko
                                                                                                                                                                                                                                                                                                                                                                                                              610 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.5%
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-525-742-8
                                                                                                                                                                                                                                                                                                                                 TELEPHONE: ZUZ-UZ-
THELEPHONE: ZUZ-8870357
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                         CURRENT APPLICATION
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APPLICANT:
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APPLICANT:
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         SOFTWARE:
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APPLICANT: Advama, Shigemi
APPLICANT: Advama, Shigemi
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
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                                                                                                                                                                                                                                                                              27 CMSITKKDANPNNGQTQLQAARMELTDLINAKARTLASLQDYAKIEASLSSAYSEAETVN 86
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                        ö
                                                                                                                                                                                     Length 615;
                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                       Score 1910; DB 2;
Pred. No. 3.9e-132;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s: NAUGHTON
1725 K Street, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5871742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Ohsawa, Ikuroh
APPLICANT: Funato, Hirono
                                                                                                                                                                                             95.3%;
            TELEFAX: 202-8870357
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
                                                                                                                                                                                                           Best Local Similarity 98.2
Matches 376; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-742-10
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Best Local S
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APPLICANT: Ohkawa, Setsuko
APPLICANT: Fujisawa, Ayumi
APPLICANT: Iritani, Yoshikazu
APPLICANT: Aridani, Shikazu
APPLICANT: Aryama, Shikemi
TITLE OF INVENTION: Poultry Mycoplasma Antigens, Gene
TITLE OF INVENTION: Thereof and Recombinant Vectors Containing the Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
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                                                                                                                                                                                                                                                                                                                                                                                                           Westerman, Hattori, McLeland &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1612; DB 1;
Pred. No. 1.3e-110;
6; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS version 5.0
SOFTWARE: ASCII from Word Perfect version 5.1
CURRENT APPLICATION DATA:
                                          327 YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
                    302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1725 K Street, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Theresa M. Stevens-Smith
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: PO-8-A930918
TELECOMMUICATION INFORMATION:
TELEPHONE: 202-659-2930
TELEFAX: 202-887-0357
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COUNTRY:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNITTER: IBM PC COMPAtible
TOWNITTER: TOWNITTER: PC-DOS/MS-DF
                                                                                                                                                      Sequence 4, Application US/08185851A Patent No. 5489430
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APPLICANT: Ohkawa, Setsuko
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NAME: Theresa M. Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 368 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-887-0357
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.4
Best Local Similarity 95.0
Matches 320; Conservative
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ADDRESSEE: Armstrong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-185-851A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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STREET: 17
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                                                                                                                                  US-08-185-851A-4
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STATE:
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            APPLICANT: Aoyama, Shigemi
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND &
ADDRESSE: NAUGHTON
STREET: 1725 K Street, Suite 1000
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FILLING DATE: 25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1638; DB 2;
Pred. No. 1.6e-112;
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95.5%; Pred. No. 1.0
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APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCLeland, Le-Nnung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 95(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 368 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                                                                                                                                                                                                                                Washington
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CLASSIFICATION:
                                                                                                                                                                                                                                                                        USA
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 114; Gaps
                                                                                                                                                                                                                                                                                    ----- 380
                                                                                                                                                                                                                    242 -----PSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYG-PSTGYLYFPYKLVKAAD 294
                                                                62 NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                     105 AKTGATLNEVNEAKTTLDAAIKKAASAKNDFDAQHGSLVEAYNNLKETLKEEKTNLDSLA 164
                                                                                                                                122 STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTN 181
                                                                                                                                                     182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE 241
                 : ||::|| : || || || || || || || 45 NTNPSDGQGMMNAAAKELADAKAALTTLINGETANLASYEDYAKIKSELTSAYETAKAVS 104
 61
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DANPNNGQTQLEAARMELTD-----LINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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APPLICANT: FOSTER, Timothy J.
APPLICANT: McDevitt, Damien L.
ATITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: US/08/293,728D
CURRENT FILING DATE: 1994-08-22
NUMBER OF SEQ ID NOS: 2.0
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0.0011;
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Staphylococcus aureus US-08-293-728-2
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Best Local Similarity 22.8%
Matches 96; Conservative
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456 PTAVTVDLLKGY 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                               PSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND ADDRESSEE: NAUGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.2%; Score 806; DB 2; I
42.8%; Pred. No. 2.9e-51;
tive 62; Mismatches 123;
                                                                                 302 YKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                     YKLNNGNVQQVEFATSTSANNTTANPTQQLMRLKLLK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/JP94/00541
                                                                                                                                                                                                                                                                                                                                                       Aoyama, Shigemi
Takahashi, Kiyoohito
/ENTION: NEW POLYPEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
APPLICATION NUMBER: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1725 K Street, Suite 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                    Sequence 2, Application US/08525742 Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 95C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                        APPLICANT: Obsawa, Ikuroh
APPLICANT: Funato, Hirono
APPLICANT: Iritani, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     Saito, Shuji
Ohkawa, Setsuko
Saeki, Sakiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J
FILING DATE: 31 "BAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-525-742-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AOYAMA, S
APPLICANT: Takahashi
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1725 K St
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Saito,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                          RESULT 5
US-08-525-742-2
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APPLICANT:
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Best Local S
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208 ANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAG-TN 266

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192 IRKQAQQPDKKEDAEVKVREELGKLFSSTKAGLDQEIQEHVKKETSSEENTQKVDEHYAN 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 TTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TVYEGEDVKFTVTAKSDSKTTLDFSDLL----TKYNPSVSDRIST 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 ITKKDANPNNGQTQLEAARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AE 58
                                                                                                                                                                                                                                    APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-19A FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
CORRESPONDENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 INNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 FSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----
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Best Local Similarity 22.7%; Pred. No. 0.064;
Matches 84; Conservative 51; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32.893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/923,992A FILING DATE: 05-SEP-1997 CLASSIFICATION: 536
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APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                    Sequence 8, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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                                         RESULT 8
US-08-923-992A-8
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THQANTPATTQSSNTNAEELVNQ-TSNETTFND--TNTVSSVNS-----PQNSTNAENV 172
                                                                          267 TKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTAN 326
                                                                                                                                                                                                                                    327 PIPAVDEIKVAKI------VLSGLRFGQNTIELSVPTGEGNMNKVAPMI-GNIYLSSNE 378
                                                                                                                                                                                                                                                                                          363 KTVLVDYEKYGKFYNLSIKGTIDQIDKTNNTYRQTIYVNPSGDNVIAPVLTGNLKPNTDS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EETPVTGEATTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSNEITTANKNINNTLSTINEQ----KTN-ADALSNSFIK----KVIQNNEQSFVGTFTN 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPAVDEIKVAKI------VLSGLRFGONTIELSVPTGEGNMNKVAPMI-GNIYLSSNE 378
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                                                                                                                                                     TKDDVKATLIMPA--YI-----DPENV-----KKTGNV----TLATGIGSTTAN 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.9%; Score 159; DB 4; Length 933;
Best Local Similarity 22.8%; Pred. No. 0.0011;
Matches 96; Conservative 57; Mismatches 154; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MSITKKDANPNNGQTQL--EAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Foster, Timothy J.
APPLICANT: Moster, Timothy J.
APPLICANT: MODEVILL, Damien L.
TITLE OF INVERTION: The S. aureus Fibrinogen Binding Protein Gene FILE REFERENCE: 05344.105011
CURRENT APPLICATION NUMBER: 08/09/421,868
CURRENT FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1994-08-22
SOFTWARE: PACENTIN NOS: 20
SOFTWARE: PACENTIN VET. 2.0
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Patent No. 6177084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylococcus aureus
US-09-421-868-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
292 AKVPP---
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                                                                                                                                                              Sequence 24, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOSSUROICE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT PAPLICATION DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENT VET. 2.0
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Gaps
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Patent No. 6284480
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Haemophilus influenzae US-09-268-347-24
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GGSYAFGNDN 774
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LENGTH: 1002
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US-09-541-782-6
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Sequence 30, Application US/09268347
; Patent No. 6335182
; GENERAL INFORMATION:
APPLICANT: LOSSIMOTE, Sheena M.
TILLE OF INVERTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
; CURRENT APPLICATION NUMBER: US/09/268,347
; CURRENT FILING DATE: 199-03-16
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 135.5; DB 4;
20.9%; Pred. No. 0.067;
Live 76; Mismatches 182;
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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US-09-268-347-30
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Matches 97; Conservative
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LENGTH: 1004
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Patent No. 6280738
GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 HSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQOKI-----ELTVSPENI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131.5; D
Pred. No. 0.15;
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FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.68;
                                                         TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            LENGTH: 1164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.8%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               TYPE: amino acid
TYPE/CAT: linear
MOLECULE TYPE: protein
US-08-923-992A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 DEIKVAKIV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672 KGELNKEYNAQVRNANE------VKFKSGNGINVSGKTLDNGTREITFELAKDEN 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tal, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-1gA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                            346 GKLAKTKVKLVSANGTNPVKISNVADGTENTDAVSFK--QLKALQD-KQVTLSASNAYAN 402
                                                                                                                                                                                                                                                                                                                                       158 ATIQDGAKTTTGLVEASELVDSLNKLGWKVGTGTDGTGVTDGTHTDTLVKSGDKVTLKAG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 -----EQRATN------LEGLSSTAYNQIRNNLVDLYNKASSLITK----TLDPLNGGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 LLDSNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSN 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSAN 321
                                                                                                                                          1 GCMSITKKDANPNNGQTQLEAARM----ELTDLINAKAMTLASLQDYAKIEASLSSAYSE 56
                                                                                                                                                                                                                                                                                     57 A-----ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTF------DN-- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 YSFVAFSADVTPVNYKYARRTVWNGDEPS-----SRILANTNSITDVSWIYSLAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 ---LTSSADNLTKQYDNAYKGLTNLDEKSKGKQTPTVADNTAATVGDLRGLGWVISADKT
                          Pred. No. 0.079;
i; Mismatches 160; Indels 180;
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COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
                                                                                                                                                                                                                                                                                                                                                                                                                                    95 ------EHPNLVEAYKAL
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APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
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20,3%; Pic.
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                                                             Conservative
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                          Best Local Similarity
Matches 100; Conserv
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TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
TITLE REFERENCE: 1038-686
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48
LENGTH: 2048
                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.5%; Score 131; DB 4; Length 1104;
Best Local Similarity 20.2%; Pred. No. 0.15;
Matches 85; Conservative 50; Mismatches 154; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 RKQAQQADKKEDAEVKVREELGKLFSSTKAGLDQQIQEHVKKETSSEENTQKVDEHYANS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL------VEAYKALKT 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFS--FSNYGP 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 IVLSGLRFGQN-TIELSVPTGEGNM-------NKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               469 ITIKNLKLNQSQTVTLKAKDDSGNVVEKTFTITVQKKEEKQVPKTPEQKHSKTEQNVPQE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 59
                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1104;
                                                    1438.0140001/RWE
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Patent No. 6335182
GENERAL INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438
TELECOMMUNICATION INFORMATION:
TELEPRA: (202) 371-2600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
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                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-923-992A-4
                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-268-347-48
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                                                                                                                            59 TVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 118
                                                                                                                                                                                                                                                                                           119 GLSSTAYNQIRNNLVDLYNKA--SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTIN 176
                                                                                                                                                                                                                                                                                                                               177 EQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 -TGSQSTSKTVYGVNGVKFTNNAETTAAIGTTRITRDKIGFARDG-DVDEKQAPYLDKKQ 514
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                                                Gaps
                                                                                           5 ITKKDAN-----PNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC Binding Forms of the Group
TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 WNGDEPSSRILANTNSI--TDVSWIYSLAGTN--TKYQFSFSNYGPSTGYLYFPYKLVKA
                                             92;
Length 2048;
Ouery Match 6.4%; Score 129; DB 4; Length 200
Best Local Similarity 21.2%; Pred. No. 0.49;
Matches 83; Conservative 60; Mismatches 156; Indels
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COUNTRY: USA

ZIP: 20005

ZIP: 20005

COMPUTER LEDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,992A

FILING DATE: 05-SEP-1997

FILING DATE: 05-SEP-1997
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438 SSSTAAELLSDSL------TFTQPN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
RECISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1438.0140001/RWE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 EISVDAKSGNV--TAPTY-NIGVKTTELNSD 599
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08923992A
Patent No. 6280738
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
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221 SADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFS----N 275
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                                                                                                                                                                                                                                                                        169 NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                   276 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 331
                                                                                                      Indels 77; Gaps
                                                                                                                                 7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET 59
                                                                     Query Match 6.3%; Score 126.5; DB 4; Length 1128; Best Local Similarity 22.5%; Pred. No. 0.33; Matches 83; Conservative 51; Mismatches 158; Indels 77;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-923-992A-6
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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rhoptry protein -	transcription regu	cell surface antig	conserved hypothet	fibrinogen-binding	surface layer prot	filamentous hemagg	hypothetical prote	hypothetical prote	membrane associate	kinesin-related pr	hypothetical prote	kinesin-like prote	hypothetical prote	rhoptry protein -	hypothetical prote
T28676	TNBYR6	T17519	AE1130	D89852	S68553	T31102	S55119	F82884	E97066	S14032	F90073	T38378	A64596	T28677	B97806
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2401	1314	820	926	989	1524	4152	719	5005	568	1073	2271	1085	1238	2269	589
7.0	6.9	6.9	6.9	6.9	6.9	6.9	6.8	6.8	8.9	9.9	8.9	6.8	9.9	6.7	6.7
139.5	138.5	137.5	137.5	137.5	137.5	137.5	137	137	136.5	136.5	136.5	135.5	135.5	135	134.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ig, G.F surfac

RESULT	п		
major	surfac	surface protein (clone pMGA1.4) precursor - Mycoplasma gallisepticum	
C; Spec C; Date	1es: M : 01-A	C.Species: MYcOpiasma galiisepricum C.Sate: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999	_
R; Mark	ham, P	540/34 5. Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Brow 5. 347-357 1004	wnin
A;Titl A;Refe	e: The rence	Figs. act. 337, 377, 237, 137, 137, 137, 137, 137, 137, 137, 1	;e11
A; Acce A; Stat	ssion: us: pr	A;Accession: S48754 A;Status: preliminary; nucleic acid sequence not shown	
A;Mole A;Resi	cule t dues:	A;Molecule type: DNA A;Residues: 1-702 <mar></mar>	
A;Cros C;Gene	s-refe tics:	A;Cross-references: EMBL:L28424 C;Genetics:	
A;Gene A;Star	A;Genetic code: SG A;Start codon: GTG	A;Genetic code: SGC3 A;Start codon: GTG	
Quer	y Matc	41.5%; Score 831.5; DB 2; Length 702;	
Matc	hes 1	best bota similarity 12.00, Fred No. 3.06.30, Matches 173; Conservative 84; Mismatches 116; Indels 39; Gaps	8;
Οy	AG 6	DANPINGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVIN 62	
QQ	68 NT		
Qy	63 NL	NLMATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 122	
qq	128 NT		
ογ	123 TA	TAYNOIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINBOKTNA 182	
QQ	188 SN	SNFATIKTNITALYQSGKDIVTKTLDPLM-GTAINLSAVSQANTNISNAVSKLETWKTNA 246	
Qy	183 DA	DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV 236	
Op	247 TV	LATSFVKEVLVKNKLTGIDT-TNNQEQPGNYSFVGXSVDVTTGSDNARPNWSFAQRKV 305	
δλ	237 WN	WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVK 291	
QQ	306 WT	SNTDILSQPQPAEGENQQSAPDVSWIYNLTGMGAKYSLTFNYYGPSTGFLYFPYKLVN 365	
δλ	292 AA	AADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVD 332	
QQ	366 55	OSDKVALEYKLNESAVKTIDFSPSQTSPVASDATRENNRSTAAPAQGSTEINPAPTLD 425	
δy	333 EI	EIKVAKIVLSGLRFGQNTIELSVP-TGEGNMNKVAPMIGNIYLSSNENNADK 383	
Q O	426 DI	KIAKVTLSNLKFGSNTIEFSVPTTAKEGTSKVAPMIGNMYLTSSDRDVNK 477	

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A;Cross-references: GB:U90714; EMBL:L28423; NID:g1905869; PIDN:AAB50152.1; PID:g19058 R:Markham, P.F.; Glew, M.D.; Brandon, M.R.; Walker, I.D.; Whithear, K.G. Infect. Immun. 60, 3885-3891, 1992 A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Title: Characterization of a major hemagglutinin protein from Mycoplasma gallisepti A;Reference number: A44793; MUID:92363591 A;Contents: S6 A;Accession: A44793 A;MuID:92363591 A;Contents: S6 A;Accession: A44793 A;Status: preliminary A;Molecule type: protein A;Residues: 26-42 <MA2> A;Note: sequence extracted from NCBI backbone (NCBIP:111017) A;Genetic code: SGC3 A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTVW-NGDEPSSRILANT----NSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADALSNSFIKKVIONNEQSFVGTFTNANVOPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                        11 NPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 744; DB 2; Length 65
42.9%; Pred. No. 2e-33;
iive 62; Mismatches 127; Indels
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Best Local Similarity 42.9%
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A;Genetic code: S
A;Start codon: G1
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                                                                                       Syonology surface protein (clone pMGAL.3) precursor - Mycoplasma gallisepticum
C; Species: Mycoplasma gallisepticum
C; Species: Mycoplasma gallisepticum
C; Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
C; Accession: $48753
R; Markham, P. F.; Glew, M. D.; Sykes, J. E.; Bowden, T. R.; Pollocks, T. D.; Browning, G. F.; FEBS Lett. 352, 347-352, 1994
A; Markham, P. F.; Glew, M. D.; Sykes, J. E.; Bowden, T. R.; Pollocks, T. D.; Browning, G. F.; FEBS Lett. 352, 347-352, 1994
A; Marcession: $48751; MUID:95010739
A; Reference number: $48751; MUID:95010739
A; Residues: I-702 <MAR>
A; Residues: I-702 <MAR>
A; Residues: I-702 <MAR>
A; Residues: EMBL:L28424; NID:9535687; PIDN:AAA62417.1; PID:9535690
C; Genetics: A; Genetic code: SGC3
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 ANNVGLQYKLNNGNVQQVEF-----SAN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 NPNNGQT----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTP-----VNYKYARRTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 NGD--EPSSRILANIN-SITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 37.6%; Score 754; DB 2; Length 702; Best Local Similarity 41.6%; Pred. No. 6.2e-34; Matches 176; Conservative 62; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA
A;Residues: 1-650 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 DKI 384
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S48751
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major surface protein (clone pWGA1.2) precursor - Mycoplasma gallisepticum (Species: Species: Species: Mycoplasma My
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62416.1; PID:9535689
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42.3%; Pred. No. 2.2e-33;
iive 62; Mismatches 125;
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major surface protein (clone pMGA1.5) precursor - Mycoplasma gallisepticum (fragment) (Species: Mycoplasma gallisepticum (C.Species: Mycoplasma gallisepticum (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The organisation of the multigene family which encodes the major cell surface. A;Reference number: $48751; MUID:95010739
A;Accession: $51560
A;Actatus: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major surface protein (clone pMGAl.6) - Mycoplasma gallisepticum (fragment)
C;Species: Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 07-Dec-1999
C;Accession: S51560; S48757
R;Markham, P.F.; Glew, M.D.; Sykes, J.E.; Bowden, T.R.; Pollocks, T.D.; Browning, FEBS Lett. 352, 347-352, 1994
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A; Cross-references: EMBL:L28424; NID:9535687; PIDN:AAA62419.1; PID:9535692
A; Orde: the sequence of residues 385-386 and the corresponding nucleotide s C; Genetics:
A; Genetics: SGC3
A; Senetic code: SGC3
A; Start codon: GTG
                                 -- NNTTANPTPAVDE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 NINATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 DANPING-----QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNN 62
                                                                         123 TA-YNQIRNNLVDLYNKASSLITKTLDPLN-GGTLLDSNEITTANKNINNTL--STINEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 KTNADALSNSFIKKVIQNNEQSFVG---TFTNANVQPSNYSFVAFSADVTP-----VNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 KYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPS-TGYLYFPYK
                                                                                                                                                                                              334 IKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                    STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 LVKAADANNVGLQYKLNNGNVQQVEF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 138; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hemagglutinin homolog pMGA1.2 - Mycoplasma gallisepticum
C;Species: Mycoplasma gallisepticum
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 07-Dec-1999
C;Accession: A49218
R;Markham, P. P.; Olew, M.D.; Whithear, K.G.; Walker, I.D.
Infect. Immun. 61, 903-909, 1993
A;Title: Molecular cloning of a member of the gene family that encodes pMGA, a hemagglut
A;Reference number: A49218; MUID:93162830
A;Status: preliminarv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 179
                                                                                                                                                                                                                                                                                                                                                                                      TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGPSTGY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA----NNTTANPTPAVDEIKVA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: sequence extracted from NCBI backbone (NCBIN:125182, NCBIP:125183)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
9 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 DANPNNGQ-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S55216; NID:g265625; PIDN:AAB25397.1; PID:g265626
A;Experimental source: S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYKYARRIVW-NGDEPSSRILANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
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Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
Molecule type: DNA; protein
Residues: 1-647 <MAR>
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C; Genetics:
A; Genetic code: SGC3
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G.F

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C; Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homolo C; Superfamily: surface-located membrane protein E; 24,Domain: signal sequence #status predicted <SIG> F; 1-24,Domain: signal sequence #status predicted <SIG> F; 25-1302/Product: surface-located membrane protein Lmp3 #status predicted <MAT> F; 95-992/Domain: tetratricopeptide repeat homology <TT1> F; 993-1026/Domain: tetratricopeptide repeat homology <TT2> F; 1089-1120/Domain: tetratricopeptide repeat homology <TT3> F; 1154-1190/Domain: tetratricopeptide repeat homology <TT3> F; 1154-1190/Domain: tetratricopeptide repeat homology <TT4>
                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JC6009
R; Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
J; Bacteriol. 178, 2775-2784, 1996
A; Title: Analysis of 0.5-Kilobase-pair repeats in the Mycoplasma hominis lmp gene sys A; Reference number: JC6009; MUID: 96213016
A; Accession: JC6009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1302 <LAD>
A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336
                                                                                                                                                                                                                                                                                                                                         C;Species: Mycoplasma hominis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                surface-located membrane protein 1mp3 precursor - Mycoplasma hominis
-----KVAPMIGNIYLSSNEN 379
                                                                              886 LOGAINDKDATLRNONYLDADES 908
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Matches 94; Conservat
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A;Genetic code: SGC3
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K.;
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Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: Obte: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
Cispecies: 189921
Cispecies: This with the content of the content
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-6713 < KUR>
A; Residues: 1-6713 < KUR>
A; Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149
A; Experimental source: strain N315
C; Genetics: A; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADVIPVNYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLA------GINTKY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AYNQIRNNLVDLYNKAS-SLITKTLDPLNG--GTLLDSNEITTANKNINNTLSTINEQKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDGATNLNKAQKDALKAQVTSAQRVANVTSIQQTANELNTAMGQLQHGIDDENATKQTQ 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                    292 AADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRFGQNTI 351
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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                                                                                                                                                                                                                                                                       Length 320;
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22.6%; Pred. No. 0.55;
Live 66; Mismatches 179; Indels
                                                                                                                                                                                                                                                                  ch 9.5%; Score 189.5; DB 2; Length I. Similarity 48.9%; Pred. No. 0.0016; 46; Conservative 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELSVP-TGEGNMNKVAPMIGNIYLSSNENNADKI 384
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                          A; Residues: 1-320 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                 280 TGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEI--KVA 337
                                                                                                                                                             NNNLNATLEQLKMAKTNLESAINQANTDKTTFDN-----EHPN-----LVEAYKAL 106
                                                                                                                                                                                       Gaps
                                                                                5 ITKKDANPNNGQ----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETV 60
                                                                                                                                                                                                                                                                                                                        EITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVA
                                                                                                                                                                                                                                                                                                                                                           ELEQTRKDIDEFINT-NKTNPNYSTLISELTSK--RDSKNSITNSSNKSDIETANTEL--
                                                                                                                     864 ITKKLETFNKDKDVKFKELEQTRKDIDEFIN----TNKTNPDYSTLISELTSKRDSKNSI
                                                                                                                                                                                                                                              107 KITLEQRAINLEGLSSTAYNQI-RNNLVDLYNKASSL-----ITKTLDPLNGGTLLDSN
                                                                                                                                                                                                                                                                                                                                                                                                       220 FSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS
                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1177 EITKKLETFNKDK------EAKFNELKKTRGQIQEFINTNKNN----PNY 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 KIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNI--YLSSNENNADKIPGY 387
8.6%; Score 173; DB 1; Length 1302;
22.8%; Pred. No. 0.08;
tive 67; Mismatches 163; Indels 8
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3890 <KUR>
A;Cross-references: GB:BA000018; PID:g13701233; PIDN:BAB42528.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                              1447 KANEQKAL------IAQTADATTEEKEQANQQVDAQLTQGN-QNIENAQSI 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3528 TDLNTAMGNLQGAINDEOTTLNS-QNYQDATPSKKTAYTNAVQAAKDILNKSNGQNK-TK 3585
                                                                                                                              1303 NDQNATNEEKEAAIQQLATAVTDAKNNITAATDDNGVDTAKDAGKNSIQSTQP---ATAV 1359
                                                                                                                                                                                                                                                                                                                               1360 KSNAKNEVDQAVTTONQAIDNTTGATTEEKNAAKDL-----VLKAKEKAYQDIL---N 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1491 DDVNTAKDNAIQAIDPIQASTDVKTNAR----AELLTEM----ONKITEILNNNETTNE 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 TNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDL 135
                                                                                                                                                                                            111 -EQRATNLEGLS-----STAYNQIRNNL------VDLYNKASSLITKTLDPLNGGTLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 ---KKVIQNNEQSFVGTFTNANVQPS-NYSFVAFSADVTPVNYKYARRTVWNGDE---- 241
                                                                                                                                                                                                                                                                                      157 DSN-----EITTANKNINNTLSTINEOKTNADALSNSFIKKVIONNEOSFVGTFTNAN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ebhB [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 TOLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEA-ETVNNNLNATLEQLKMAK 75
                                    266 NTKYQFSFSNYGPSTGYLYFPYKLVKAADAN------NVGLQYKLNNGNVQQVEFATST
       9 DANPNNGQTQLE------AARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE
                                                                                                 59 TVNNNLN-----ATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTL--
                                                                                                                                                                                                                                                                                                                                                                                210 VQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIYSLA----GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 SANNTTA-NPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3586 DQVTEAMNQVNSAKNNLDG----TRLLDDQAKQTAKQQLNNMTHLTTAQKTNLTNQ----
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24.4%; Pred. No. 1.1;
tive 54; Mismatches 153;
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Best Local Similarity 24.48
Matches 94; Conservative
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C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D90011
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2422
A;Status: preliminary
A;Molocule type: DNA
A;Residues: 1-661 <KUR>
A;Residues: 1-661 <KUR>
A;Coss-references: GB:BA000019; PIDN:BAB76634.1; PID:g17134073; GSPDB:GN00179
C;Genetics: A;Cene: all4935
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A;Cross-references: GB:BA000018; PID:g13701961; PIDN:BAB43253.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 NLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALSNSFI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 LKMAKTULESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATULEGLSSTAYNQIRN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 NTAIAELDQANTRLNTARN-----DFNTANSNFSRTGNELNTAINNFNTANNTFNTATT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LNTATNNRNNAQNALNTATNNRDN-----AQNALNTATNNR-NNAQNALNTATNN-RN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------NTALNTATNNF 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LEAARMELTDLI-----NAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQ 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 8.2%; Score 164.5; DB 2; Similarity 23.1%; Pred. No. 0.55; 98; Conservative 56; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                   40; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNNFST-----ANTAFNTATNNFSTA-----
                                                                                                                                                                                                                                                                                                                                       8.3%; Score 165.5; DB 22.7%; Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 NFNN--ASSRRNTAEQARNOVREETRL 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 MIGNIYLSSNENNADKIPGYRRPGTFL 394
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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Best Local S
Matches 98
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Length 3890; Indels . ж

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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471
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A86827
hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL140
hypothetical protein yqfG [imported] - Lactococcus lactis (strain IL140
C)species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: A86827
                                                                                                                                                                                                                     A;Cross_references: GB:AE001420; GB:AE001362; NID:g3845287; PIDN:AAC71959.1; PID:g384
A;Experimental source: clone 3D7
C;Genetics:
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71605
E;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A1600; MUID:99021743
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A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
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                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 168
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21.0%; Pred. No. 0.6;
tive 76; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                         7.8%; Scc. No. v.. 23.8%; Pred. No. v.. .. 48; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Conservative
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Matches 97; Conservat
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Best Local Similarity
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746 NNLTTSN 752
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                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: clumping factor
C; Species: Staphylococcus aureus
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999
C; Accession: S41539; S36630
R; McDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.
Mol. Microbiol. 11, 237-248, 1994
A; Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Stap
A; Accession: S41539
A; Accession: S41539
A; Satus: preliminary
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                                                                                                                                                                 NNDKQTAYNNAVAAAETIINANSNPEMNPSTITQKAE--QVN---SSKTALNGDENLATA 3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-933 <MCD>
Cross-references: EMBL:218852; NID:g397525; PIDN:CAA79304.1; PID:g397526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TINGANTPATIQSSNINAEELVNQ-ISNETIFND--INIVSSVNS-----PQNSINAENV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SST-----AYNQIRNNLVDLYNK------ASSLITKTLDPLNGGTLL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKDDVKATLTMPA--YI-----DPENV-----KKTGNV-----TLATGIGSTTAN 362
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                                                          242 -PSSRILANT-NSITD-----VSWIYS---LAGTNTKYQFSFSNYGPSTGYLYFPYKLV
                                                                                                                                         291 KAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDE-IKVAKIVL---SGLRF
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                                                                                3738 KQNAKTYLNTLTSITDAQKNNLISQISSATRVSGVDTVKQNA---
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0.3;
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                                                                                                                                                                                                                                               3836 AQNAVEAALQRVNTAKDALNGDAKLI 3861
                                                                                                                                                                                                                         GONTIELS --- VPTGEGNMNKVAPMI 369
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N;Alternate names: clumping factor
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2004
1. GCMSITIKKDANPNNGQTQLE......SSNENNADKIPGYRRPGTFL
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SW11_YEAST
YM41_YEAST
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Y338_MYCGE
BAG_STRAG
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P2P_LACLC
ALS1_CANAL
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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09pjy2	P38272	004893	954001	009625	P49022	P41508	P28742	002470	002945	P25146	P11657
PMPB_CHLMU	YBYO_YEAST	YM96_YEAST	TOLC_SALEN	YS8A_CAEEL	PIP_LACLA	P115_MYCHR	KIP1_YEAST	P2P_LACPA	VP4_ROTEH	INLA_LISMO	PAC STRMU
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                            13;
                                                                 MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                            | | | | : : : | : : | | : : | : : | : : | : : | EMKVSLQETQVSSE----FSKRDSVINKEAVPVSKDELLEQSEVVVSTSSIQKN-KILDN 148
                                                                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                                                                                 149 KKKRANFVISSPLIKEKPSNSKDASGVIDNS-------ASPLSYRKAKEVVS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                          ------WNGDEPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                             58 ETVNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARG5.6 protein, mitchondrial precursor [Contains: N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase); Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase)].
                                                                                                                                                          NISIN LEADER PEPTIDE PROCESSING SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 LRQPLKNQKVEAQPLLISNSSEKKASVYTNSHDFWDYQW------DMKY---VTNNGES
                                                                                                                                                                                                                                                                                                                                          QKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTV~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KMGHGTEVAGQITANGNILGVAPGITVNIYRVFGEN
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D5F29313F2983EC9 CRC64;
                                                                                                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                            61; Mismatches 130;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                          7.7%; Score 154.5; D
21.0%; Pred. No. 0.11;
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   email to license@isb-sib.ch)
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                                                         InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR000209; Peptidase_S8.
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                    EMBL; L11061; AAA25200.1; -. EMBL; X76884; CAA54210.1; -. HSSP; P29600; 1GCI.
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ses 75; Conserv
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                                                  MEROPS; S08.059;
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P78586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autopology 143:297-302(1997).

-i- CATALYTIC ACTIVITY: N-acetyl-L-glutamate 5-semialdehyde + NADP(+)

-i- Phosphate = N-acetyl-5-glutamyl phosphate + NADPH.

-i- CATALYTIC ACTIVITY: ATP + N-acetyl-L-glutamate = ADP + N-acetyl-L-

-i- PATHWAY: SECOND AND THIRD STEPS IN ARGININE BIOSYNTHESIS.

-i- PATHWAY: SECOND AMICOPATION: MICOCHORAIAI.

-i- SUBCELLULAR LOCATION: MICOCHORAIAI.

-i- SUBLIARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 K----TTFDNEHPNLV-EAYKALKTTLEQR-----ATNLEGLSSTAYNQIRNNLVDLYNK 138
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                                                                                                                                                                                                                                                                                                                                          Nombela C.;
of the ARG5,6 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLGLUTAMATE KINASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE NAGSA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 134;
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE
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TRANSIT

ACETYLGLUTAMATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%; Score 143; DB 1; Length 857;
23.3%; Pred. No. 0.64;
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BY SIMILARITY.
AE2CEAD8FF8C4C71 CRC64;
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                                                                                                                                                                                                                                                                                                                                     Negredo A., Monteoliva L., Gil C., Pla J., "Cloning, analysis and one-step disruption Candida albicans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD003765; AGPR_act_site; 1. PROSITE; PS01224; ARGC; 1.
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InterPro; IPR001048; Aakinase.
InterPro; IPR000534; Semialdh_dh.
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Pfam; PF01118; Semialdhyde_dh; 1.
Pfam; PF02774; Semialdhyde_dhC; 1.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ATCC 64385 / 1001;
MEDLINE-97195775; Pubmed-9043106;
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857 ?
                                                                                                              NCBI_TaxID=5476;
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RESULT 4
YM41_YEAST
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Matches
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                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription regulatory protein. SWII (SWI/SNF complex component SWII)
(Transcription regulatory protein DARE) (Regulatory protein GAM3).
ADRE OR SWII OR GAM3 OR YPL016W OR LPAI.
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 ---KLVKAADANNVG--LQYKLNNG---NVQQVE-FATSTSANNTTANPTP 329
                                                        AVDEIKVA----KIVLSGLR--FGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
                                                                                                                                                                                                                                                                                                                        MEDLINE-89057455; PubMed-3143101;
O'Hara P.J., Horowitz H., Elchinger H., Young E.T.;
"The yeast ADR6 gene encodes homopolymeric amino acid sequences and potential metal-binding domain.";
Nucleic Acids Res. 16:10153-10170(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            franscription regulation; Activator; DNA-binding; Nuclear protein;
                    LFWYGLNIDEASKLIKEFDSSSIGSSLSSSKESGVFTSAQQKRGFHHSTVRRNT--NPNP
                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 65 ASN/THR-RICH.
337 385 GLN-RICH.
1241 1258 C4-TYPE.
1314 AA; 147938 MW; F442D5A82013CDBD CRC64;
                                                                                                                                                                                                                                                                               Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                  PRT; 1314 AA.
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                                                                                                                                                                                       (Rel. 10, Created)
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InterPro; IPR001606; ARID.
Pfam; PF01388; ARID; 1.
SWART; SW00501; BRIGHT; 1.
                                                                                                                                                                  STANDARD;
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CHARACTERIZATION.
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284 YFPY----
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                                                                                                           575 QGYNK 579
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P09547;
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                                                                                                                NPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQ 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 TPHFITN--VQSISQNSSSSTPN--TNSNSTPNANQQFLPFNNSASN-----NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 NADALSNSFIKKVIQNNEQSFVGTFTNANVQP-SNYSFVAFSADVTPVNYKYARRTVWNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
  Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 79.4 kba protein in ALD2-DDR48 intergenic region.
YMR172W OR YM8010.02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MSITKKDANPNNGQTQLEAARMELTDL-------INAKAMTLAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
Submitter C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JUN 1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175; Indels
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4652BE93743D5A54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 LOYKL------NNGNVQQVEFATSTSANNTTANPTPAVDE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                        126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 137; DB 1;
19.8%; Pred. No. 1.1;
Live 72; Mismatches 175
6.9%; Score 138.5; D
20.4%; Pred. No. 1.9;
iive 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 719 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79415 MW;
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGD; S0004783; YMR172W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 719 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                Similarity
     Query Match
Best Local Sim:
Matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YM41_YEAST
Q03213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCCean J., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: COULD BE A SPINDLE POLE BODY WORDR. ON TRANSITION FROM
G2 TO M PHASE OF THE CELL CYCLE, THE SPINDLE POLE BODY DUPLICATES;
THE DAUGHTER POLE BODIES SEED MICROTUBLIES WHICH INTERDIGITATE TO FORM A SHORT SPINDLE THAT ELONGATES TOSPAN THE NUCLEUS AT
METAPHASE. MUTATIONS AT CUT7 BLOCK SPINDLE FORMATION.
-!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 NDHASAAQKPISALSPLINSHNSTISMNYINSSIHSGYISASNSFHDLNSLNNFGTITAL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SRILANTNSITDVSWIYS-----LAGTNTKYQF-SFSNYGPSTGY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANPTPAVDEIKVAKIVLS 342
                                                            97 LLRTSAAISAPTGTSQPTETIGEKLSNEERVNSNVSASNSTTAGTGRMLSQSLTN-DSPS 155
                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                              -----INNTLSTINEQKTNA--------DALSNSFIKKVI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-91015362; PubMed-2145514;
Hagan I., Yanagida M.;
"Novel potential mitotic motor protein encoded by the fission yeast
                                                                                                                                                                                         216 KLVAQPSARPSTNNAQNKLAIELLNSISAVSSAYLQKMQNNGSGRQHTADLCTGDSNTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NQIRNNL-VDLYNKASSLITKTLDPL--NGGTLLDSNEITTANKN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GINQHRTTNGTIDVNTNTAQLNNQFSNALNTILPDQQHNRNNVSQNINQSLPNRQLGPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----QNNEQSFV-GTFTNANVQPSNYSFVAFSAD----VTPVNYKYARRTVWNGDEPS-
----TLEQLKMAKTNLESAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 SLPSLALDNASFPPNQNVIPPIINNTOOPLSFSQLINQDSTTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 GLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRPGT
                                                                                                                                       NQANTDK - - - - TTFDNEHPNLV - - - EAYKALKTTLEQRATNLEGLSSTAY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
       -LQDYAKIEA-----SLSSAYSEAETVNNLNA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinesin-like protein cut7. CUT7 OR SPAC25G10.07C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
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P24339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 QVE----FATSTSANNTT------ 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEQLKMAKTNLESAINQANTDKTTFDNEHPN-----LVEAYKALKTT----LEQRATNLEG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 LQHTHEESQKELMYGVRNDIDALVKTCTTSLNDADIILSDYISDQKSKFESKQQDLIANI 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 NGYFTLLNDFNASMEELLNTHSNQLLISMTKITEHFQSLDEALQSARSSCAVPNSSLDLI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    683 VSELKDSKNSLLDALBHSLQDISMSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYN 742
                                                                                                                                             PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Cell division; Microtubules; ATP-binding; Coiled coil;
Mitosis; Cell cycle; Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 NGQ-TQLEAARMELTDLINAKA-MTLASL----QDYAKIEASLSSAYSEAETVNNNLNAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVNLEVQTLDRLLQKVKEHSEDNTKEKHQQL---LDLLESLVGNNDNLIDSIKTPHTELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 YSFVAFSADVTPVNYKYARRTVWNG----DEPSSRILANTNSITDVSWIYSLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKNINNTLSTINEQ-KTNADAL----SNSFIKK---VIQNNEQSFVGTFTNANVQPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTNTKYQ-------QYKLNNGNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 LSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEIT------
                                                                                                                                                                                      Phosphorylation; Repeat.
StringsIN-MOTOR (BY SIMILARITY).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                         SIMILARITY)
SASNPRKREBPTIDTGYPDRSDTNSPT
LRAILGNDVSLLLTL (IN REF. 1).
MW, 5669277875559D58 CRC64;
                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352. ---- ELSVPTGEGNMNKVAPMIGNIYLSSNENNADKIPGYRRP 390
                                                                                                                                                                                                                                                COILED COIL (POTENTIAL)
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 135.5; DB 1;
20.9%; Pred. No. 2.2;
tive 76; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MG338 precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1271
or send an email to license@isb-sib.ch)
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(Rel. 33, Last sequ
(Rel. 40, Last anno
                                                                                                                  PRINTS; PR00380; KINESINHEAVY
                                                                                  InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
                           EMBL; X57513; CAA40738.1; -. EMBL; Z70691; CAA94636.1; -.
                                                                                                                                                                                                                                                                                                                                                                   1085 AA; 122133
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                 SM00129; KISC;
                                                         PIR; S14032; S14032.
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                         HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                          34
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01-FEB-1996 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
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P47580;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                  NP_BIND
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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Y338_MYGGE
ID Y338_M
AC P47580
DT 01-FEB
DT 16-OCT
DE Hypoth
                                                                                                                                    SMART;
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                          DOMAIN
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252 SIT--DVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNV 309
                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00746; Gram_pos_anchor; 1.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION OF IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                             Mol. Microbiol. 5:843-849(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1164 AA; 131051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X59771; CAA42442.1; -.
                                                                                                                                                                                                                                       Streptococcus agalactiae.
                                                   310 QOVEFATSTSANNTTANPT
                                                                          584 DVCDLAKKLLKNNTNLSET
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain
                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1311;
                                                                                                                                                                                                                                                                                                                                                                                   binding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
439
827
1131
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                                                                                                                                            BAG_STRAG
P27951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                 Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Eritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANK--NINNTLSTIN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 GTSSNL-----NPLDKFIKSSSATTVAMK----SAMTKSQEVTSDNNGFNVKSEFLKIN 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E--QKTNADALSN--SFIKKVIQNNEQSFVGTFTNANVQPSNYS------FVAFSAD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | : | | : | | TT---QKQQQKPVYVRGDDAIYAFHIDGGNYFLENSSPNKRNFEKQAEVLLMRFLQGGTN 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLSSSGSDNSSNTQSFWKQVQALNNSSQTATIFDAVRMESNSSQAQVVTSNLLVSLSSK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                       sequencing.";
J. Bacteriol. 175.7918-7930(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 KDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAK-IEASLSSAYSEAETVNNNLNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 LLDFENKYSASKVLISKNNILSVLKTVNLSAAVIDQYH-YLLNNKTELTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 VTPVNYKYARRTVW-NGDE-----ILANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                            Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                         Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL LIPOPROTEIN MG338.
N-ACYL DIGLYCERIDE (POTENTIAL).
W; FCE6042067310A70 CRC64;
                                                                                                                                                                                                                                                                                                                                             (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%; Score 132; DB 1; Length 1271; 22.2%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                         STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
                                                                                                                                                                                                                                               STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
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                                                                                                                                                                                                                                       SEQUENCE OF 1023-1114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39715; AAC71563.1; -.
                                      Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142492
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1271
27
              4ycoplasma genitalium.
                           Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                             SEQUENCE FROM N.A.
                                                   NCBI_TaxID-2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                        sequencing.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91312121; PubMed=1857207; Jerlakroem PG., Chhatwal G.S., Timmis K.N.; Jerlakroem PG. at antiqen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGA-BINDING (POTENTIAL).
IGA-BINDING (POTENTIAL).
PRO-RICH REPEATS.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
533 NFSKDNVSFSVDLFGSNSEFR-SWANRN-TTLKLYTALTTMLENGTSN------NNGQK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGA FC RECEPTOR.
EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65DE94AF720A5474 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [gA FC receptor precursor (Beta antigen) (B antigen).
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                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                               1164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 38-48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S15330; FCSOAG.
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003599; Ig.
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Indels 122;

70; Mismatches 140;

Conservative

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89;
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  Matches
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                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SADVIPVNYKYARRIVWNGDEPSSRILANTNSITDVSWIYSLAGINTKYQFSFS----N 275
                                                                                                                                                                                                                                                                                                                                                                488 YKTNTDNHKIAEITIKNLKLNESQTVTLKAKDDSGNVVEKTFTITVQKKEEKQVPKTPEQ 547
                                                                                                                                                                                                                                                      396 HSKLKQVVEDFRKKFKTSEQVTPKKRVKRDLAANENNQOKI-----ELTVSPENI---- 445
                                                                                                                                                                                                                                                                                                   446 ------TVYEGEDVKFTYTAKSDSKTTLDFSDLL----TKYNPSVSDRISTN 487
                                                                                                                                                                                                                                                                                                                                        276 YGPSTG---YLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP-TPAV 331
                                                                                                                                                                    TLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNI 168
                                                                           Gaps
                                                          7 KKDANPNNGQTQLEA-ARMELTDLINA-KAMTLASLQDYAKIEASLSSAYSE----AET
                                                                                                                                                                                             SLEQVEKELKHNSEA-----NLEDLVAKSKEIVREYEGKLNOSKNLP--ELKQLEEEA
                                                                                                                                                                                                                             NNTLSTINEQ-----KTNADALSNSFIKKVI---QNNEQSFVGTFTNANVQPSNYSFVAF
                                77;
    Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129; DB 1; Length 1251; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax (strain Belem).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                 Indels
                                                                                                                   60 VNNNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNL----
     6.6%; Score 131.5; DB 1; 22.8%; Pred. No. 4;
                                 51; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Reticulocyte binding protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1251 AA
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                                    84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   332 DEIKVAKIV 340
                                                                                                                                                                                                                                                                                                                                                                                                                              548 KDSKTEEKV 556
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                       Best Local Similarity
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Q00799;
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SEQUENCE
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RBP2_PLAVB
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Query Match Best Local Similarity

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PSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANN-----TTA-- 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NPTPAVDE----IKVAK-----IVLSGLRFGONTIELSVPTGEGNMNKV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 VGIKITPELALFELLGDAKLKTAQELKFESKNNVVLETENMSKNTNELDVHKNIQDAYKV 791
                                                                                                                                                                                                                                                                                                                                                         518 SKGNYEIGFLEKLEEIGKNRKLKVDITKKS---INSTVG--NFSSLFNNFDLNQYDFNKN 572
                                                                                                                                                                                                                                                                                                                                                                                                                                     168 INNTLSTINEQKTNADALSNSF---IKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 TPVNYKYARRTVWNGDEPSSRILANTNSITDVSWIY----SLAGTN---TKYQFSFSNYG 277
                                                                                                                                            LEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQ 127
                                                                                                                                                                                                                        517
                                                                                                                                                                                                                                                                                             IRNNL----------VDLYNKASSLITKTLDPLNGGTLLDSNEIT--TANKN 167
QTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAE-----TVNNNLNAT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.; "Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci."; Microbiology 141:337-343(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 LRLEAQKEKVNLLNKEEEANKYLRDVKKVESFRFIFNMKESLDKINEMIKKEQLTVNEGH
                                             470 LEKVKDDOSNYVNYLNOITTER-----NLIVTEKNRLNGIDSTITNIEG----ALKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168 / BGSC1A1;
MEDLINE=97124196; PubMed=8969509;
Yoshida K. I., Shindo K., Sano H., Seki S., Fujimura M., Yanai
Miwa Y., Fujita Y.,
"Sequencing of a 65 kb region of the Bacillus subtilis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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Last annotation update)
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STRAIN=168 / BGSC1A1;
MEDLINE=95219088; Pubmed=7704263;
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(Rel. 30, Last seq
(Rel. 41, Last anno
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SEQUENCE FROM N.A.
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                                                                                                               SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
        covering the gnt-sacxY region.";
Microbiology 142:31123(1996).
-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
-!- FUNCTION: STILL UNKNOWN. NOT DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
-!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
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31 x 21 AA APPROXIMATE TANDEM REPEATS OF
44)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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1 28 OR 32 (POTENTIAL)
29 2334 WALL-ASSOCIATED PROTEIN.
504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.
                                                                                101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THI
C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
containing the lic and cel loci, and creation of a 177 kb contig
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EMBL; D31856; BAA06556.1; -.
EMBL; D29985; BAA06260.1; -.
EMBL; D83026; BAA11683.1; -.
EMBL; 299124; CAB15959.1; -.
PIR; S32920; S32920.
Subtilist; BG10797; wapA.
Interpro; IPR003305; CBD_6.
Pfam; PF02018; CBD_6: 1.
Cell wall; Repeat; Signal; Comp
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Garrison K., Mackrell A.J., Fessler J.H.;
Garrison K., Mackrell A.J., Fessler J.H.;
"Drosophila laminin A chain sequence, interspecies comparison, and domain structure of a major carboxyl portion.";
J. Biol. Chem. 266:22899-22904(1991).
-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
                                                                                                                                                                                                                                                                     1772 SVVNKEQNTTKKRTFDNKNRLTELTDRGGSQTWTYPSDSDKLK---TFSWIHGDQKGTNQ 1828
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                            -----EAYK----ALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPL 150
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                                          Gaps
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                                          113;
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MEDLINE-93049203; PubMed-1425586;
Kusche-Gillberg M., Garrison K., Mackrell A.J., Fessler L.I.,
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                                          Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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6.4%; Score 128.5;
22.1%; Pred. No. 14;
iive 56; Mismatches
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MEDLINE-94038678; PubMed-8223265;
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LANA OR LAMA.
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EMBO J. 11:4519-4527(1992).
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                     Best Local Similarity
Matches 91; Conserv
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       CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
MITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
COMPLETE LOSS-OF-FUNCTION DIVERSE FUNCTION BURRIG MORPHOGENESIS IN DROSOPHILA.
COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC
LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE
TO ESCAPER ADDITS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES
IN CELL FATE AND PATTERN, MISSHAPPEN LEGS AND DEFECTS IN WING
STRUCTURE.
DIFFERENT POLYPEPTIDE CHAIRS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISJULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRESING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
COMPRESING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
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PROSITE; PS01022; EGF_1; 17.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled Laminin EGF-11ke domain; Cell adhesion; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMININ ALPHA CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M96388; AAA28662.1; EMBL; M96388; AAA28662.1; EMBL; M96388; AAA28662.1; EMSP; P02468; AAA28661.1; EMSP; P02468; 17LE.
FlyBase; FB901002526; LanA.
InterPro; IPR00186; LanMI.
InterPro; IPR00186; Laminin_EGF.
InterPro; IPR00199; Laminin_EGF.
InterPro; IPR00199; Laminin_EGF.
InterPro; IPR00199; Laminin_EGF.
InterPro; IPR00199; Laminin_EGF.
InterPro; IPR00191; Laminin_EGF.
Ffam; PF00052; laminin_EGF; 20.
Ffam; PF00054; laminin_EGF; 20.
Ffam; PF00054; laminin_EGF; 20.
Ffam; PF00055; laminin_EGF; 20.
FroDom; PD002081; Laminin_EGF.
SMART; SM00180; EGF_Lam; 17.
SMART; SM000281; Laminin_EGF_IRE; 1.
SMART; SM000281; Laminin_EGF_IRE; 1.
SMART; SM000281; Laminin_EGF_IRE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3712
3712
372
332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 SVSQSSSSASDVSSSVSQSSSSASDVSSSVSQSASSASD-----VSSSVSQSASSTSD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 LNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSST 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNAD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 GSVNNGEIN--------LDNGSTYVIVEPVSGKGTVNIIS---GNLYLHYP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 GSQSVSS----ASGSSSSFPQST----SSASTASGSATSNSLSSITSSASSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ALSNSFIKK------VIQNNEQSF---VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATASNSLSSSDGTIYLPTTTISGDLTLTGKVIATEGVVVAAGAKLTLLDGDKYSFSADLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 TFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDE----PSSRILANTNSITDVSWIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 VYGDLLVKKSKETYPGTEFDISGENFDVTGN--FNAEESAATSASIYSFTPSSFDNSGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLSLSKSKKGEVTFSPYSNSGAFSF-----SNAI-----LNGGSVSGLQRRDDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLA-GINTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATST-
                                                                                                                                                                                                                                                               POTENTIAL.
HYPOTHETICAL PROTEIN YLLUDGE.
HYPOTHETICAL PROTEIN YLLUDGE.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 106.1 kDa protein in GLX1-GDA1 intergenic region.
YEL043W OR SYGP-ORF14.
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 995;
   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO F63E287A03F137EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Conservative 100; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                        SGD, S0001431; YIL169C.
InterPro: IPR0040099; Chemotaxis_transducer.
InterPro: IPR0040727; T_SNARE.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 DTFTGQTVVFKGEGVLAVDPTETNATPIPVVGY 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SSNENNADKIP--GY 387
                                                                                                                                                                                                                                                                                                                                                                                                                Score 128;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                 ¥
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.4%;
Best Local Similarity 16.1%;
                                                                                                                                                                       EMBL; Z46921; CAA87023.1; -.
                                                                                                                                                                                                                                                                                        28
35
468
664
99735 M
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664
695 AA;
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P32618;
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2692 -KLLATRINLSTYFRTTEPS-GFLLYLGNDNKTAQKNNDFVAVEIVNG----YPILTIDL 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2746 GNGP-----ERITSDKYVADGRWYQAVVDRMGPNAKLTIREELPNGD-----VVEHS 2792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2502 TDLLQRARQSLQKVQD--DLEPRLNASAGKVQKISAVNNATEHQLK----DINKLIDQLP 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIR-----NNLVDLYNKA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALSNSFIKKVIQNNEQ 199
                                                                                                                                                                                                                                                                                                                                                                                27 TDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNATLEQLKMAKTNLESAINQ-- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĄΣ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- ENLKAQVEAARQLANSIKV-GVNFK-------PSTILELKTPEKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 YSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANNTTANPTPAVDEIKVAKIVLSGL-----RFGQN---TIELSVPTGEGNMNKVAPMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2612 VSQANKQLDDVEGSV----SKLNELAEDIEEQQHRVGSQSRQLGQEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARRTVWNGDEPSSRILANTNSITDVSWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C / AB972;
STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser i
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones I
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                               DB 1; Length 3712;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 99.7 kDa protein in SDL1 5'region precursor.
YIL169C OR Y19402.07C.
                                                                                                                                                                                                                                                                                                                                              155;
                                              SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                               ; Pred. No. 24;
48; Mismatches
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                                                                                                                                                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                            Score 128.5;
Pred. No. 24;
                                                                                                                                                       SIMILARITY
                                                                                                                                                                                         SIMILARITY
                                                                                                                                     SIMILARITY
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                                                                                                                                                                                                                                                                             SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 GNIYLSSNEN--NADK----IPGYRRPG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
   6.48;
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.4
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                  14447
1463
11480
11487
11511
11526
11533
11544
11562
11874
11885
11896
 1408
1423
1423
1438
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DISULFID
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YIQ9_YEAST
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IDENTIFICATION
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GPI-ANCHOR
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Q12355;
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PST1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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| 503 EKNRSSGSIQLPLSNNMSRTGSIDLISNNNKSIN--NSNADSAPPLRLHNPVSYSPSNEP 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YARRIVWNG---DEPSSRILA-----NTNSIIDVSWIYSLAGINTKYQFSFSNYG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETVNNNLN-ATLE-----QLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 ITKKDANPNNGQTQLEAARMELTDL-----INA-KAMTLASLQDYAKIEASLSSAYSEA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                 STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chenr B., Cherry J.M. (duzman E., Hartzell G., Hunicke-Smith S., Chung E., Duncan M., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Nanath A., Norgren R., Oeffner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelcon M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVLKKLNDFTLEKNGFLSNAGEEFLSKLNADSSLIKMIKQELSIDQE---LEANWKLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTL-DPL--NGGTLLDSNEITTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNILKKISALE-----NQF--NEMSLNNR--NLKTKLMVQFYKNNGDSLAATNSNNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SNSFIKKVIQNNE-QSFVGTFTNAN----VQPSNYSFVA-----FSADVTPVNYK
                                                                                                                                                                                                                                                                                                                                                                                                           ### PEDELINE | PEDEC |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.3%; Score 127; DB 1; Length 956;
19.7%; Pred. No. 5.5;
tive 86; Mismatches 163; Indels 176;
                                                                    ς.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURT. BIOL. 6:1544-1546(1996).
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----INNTLSTINEQKTNADAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III.
                                                                  Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., I
Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 956 AA; 106132 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0000769; YEL043W.
InterPro: IPR003961; FN_III.
Pfam; PF00041; fn3; 1.
SMARY; SM00060; FN3; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.7%
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S30834; S30834
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                                                         SECUENCE FROM N.A.
               NCBI_TaxID=4932;
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MEDLINE-20469049; PubMed-11016834;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terashima H., Yabuki N., Arisawa M., Hamada K., Kitada K.;
Terpona encoding glycosylphosphatidylinositol
"Up-regulation of genes encoding glycosylphosphatidylinositol
disruption of FKS1 in Sacharomyces cerevisiae.";
Mol. Gen. Canton: ATACHED TO THE MEMBRANE BY A GPI-ANCHOR AND
SECRETED BY REGENERATING PROTOPLASTS.
--- SIMILARITY: BELONGS TO THE SPS2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96381250; PubMed=8789263;
Brandt P., Ramlow S., Otto Brandty S., Otto S., Otto Brandty S., Stones analysis of a 32,500 bp region of the right arm "Nucleotide sequence analysis of a 32,500 bp region of the right arm of Saccharomyces cerevisiae chromosome IV.";
--PSTGYLYFPYKLVKAADANNVGLQYKLNNGNVQ 310
                                                                         678 KGFTIDELDNYWIKOOPQVRSINESLESTIGIPMSSYK-----ANPVISPY--SSSHLR 729
                                                                                                                                                                                                                        730 QTSNATNIPMHPQSLLAATLNDPSLQSFVRSGSFYSAPQPANSLQNNINGNETENISPR 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protoplast secreted protein 1 precursor.

PST OR YDR055W OR D4214 OR YD9609.09.

Saccharomyces cerevisiae (Bakert's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
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Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       790 ISSDENLLVPNLSPRLSNDVPIVPGNNTTLTPSHSNILTMNHQPTADNI 838
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on update)
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                                                                                                                                                              311 QVEFATSTSANNTTANPTPAVDEIKVAKIVLSGLRF-
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16-OCT-2001 (Rel. 40, Last sequence up
01-WAR-2002 (Rel. 41, Last annotation
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COMPLUYEAST-2DPAGE; Q12355;
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TSFAADSLESITDSLNLQSLTILT-----SASFGSLQSVDSIKLITLPAISSFT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSS--TAYNQIRNNLV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                 SNIKSANNIYISDTSL-----QSVDGFSALKKVNVFNVNNKKLTSIKSPVETVSDSLQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLYNKASSLITKTLDPL---NGGTLLDSNEITTANKN-----INNTLSTINEQKTNA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VIQNN------EQSFVGTFIN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 IGQTFSIVSNDYLKNLSFSNLSTIGGALVVANNTGLQKIGGLDNLTTIGGTLEVVGNFTS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 SVKLSSTSKSOSS-----QTTAKVSKSSSKAEEKKFTSGDIKAAASASSVSSSGASS-- 410
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                                                                                                                                                                                                                                                                                                                     Indels 105; Gaps
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01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86136024; PubMed=3004972; Mackay M., Gomman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.; Paljard H.; Peljymorphism of the precursor for the major surface antigens of
PROTOPLAST SECRETED PROTEIN 1. REMOVED IN MATURE FORM (POTENTIAL)
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5839;
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Matches 73; Conserv
                                                                                                                                                                                                                                                444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                      PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 KVIQNNEQSFVGTFTNANVQPSNYSFV-----AFSADVTPVNYKYARRTVWNGDEPS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- TNSITDVSWIYSLAGTNTKYOFS 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 VGKMEDYIKKNKKTIENINELIEESKKTIDKNKNATKEEEK-----KKLYQAQYDLSI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 YNKQ---LEEAHN-LISVLEKRIDTLKK-----NENIKELLDKINEI--KNPPPAN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 GG----TLLDSN-EITTANKNINNTLSTINEQKTNADAL-----TLLDSN-EITTANKNINNTLSTINEQKTNADAL-----
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                                                                     Pan W., Tolle R., Bujard H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNTPNTLLDKNKKIEEHEKEIKEIAKTI---KFNIDSLFTDPLELEYYLREKNKNIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 AKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINPFDYT------KEPS
Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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20.7%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A. MEDILINE-8601435; PubMed-2995820; MEDILINE-8601435; PubMed-2995820; Hablder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).

-1. PPH: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holder A.A.; Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P195).
                 (POTENTIAL)
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2C255B6616C87F6E CRC64;
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Pfam. PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                 "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites."; Nature 317:270-273(1985).
328 TPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK
                                                                                                                                                                                                                                  plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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N-LINKED (GLCNAC. . ) (POTE
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                                                                                                              STANDARD;
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                                                                                                              MSP1_PLAFW
P04933;
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Gaps

Indels 113;

Length 1639;

DB 1;

Pred. No. 11; 2; Mismatches 155;

62;

Conservative

86;

Query Match Best Local S Matches 86

Similarity 20.7%; Pred. No. 11;

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192 KVIQNNEQSFVGTFTNANVQPSNYSFV-----AFSADVTPVNYKYARRTVWNGDEPS 243
                                                                                                                                                                                                                                                                 390 AKVETKESTEPNEYPNGVTYPLSYNDINNALNELNSFGDLINFPDYT-------KEPS 440
                                                                                                                                                                                                                                                                                                                    -----TNSITDVSWIYSLAGINTKYQFS 272
                                                                                                                                                                                                                                                                                                                                                       441 KNIYTDNERKKFINEIKEKIKIEKKKIESDKKSYEDRSKSLNDITKEYEKL-LNEIYDSK 499
                                                                                                                                                                                                                                                                                                                                                                                              273 FSNYGPSTGY----LYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTANP 327
                                                                                                          ---SNSFIK 191
                            92 FDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYNQIRNNLVDLYNKASSLITKTLDPLN 151
  91
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053653 stephylococ
04945 mycoplasma
096662 plasmodium
09cf64 lactococcus
09pq08 ureaplasma
04955 mycoplasma
049169 stephylococ
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09161 stephylococ
09161 stephylococ
04948 mycoplasma
04954 stephylococ
026109 plasmodium
0911p9 mycoplasma
095489 helicobacte
095489 helicobacte
                             Q99u54 staphylococ
Q93lr6 staphylococ
Q49547 mycoplasma
                                                                   Q99qr6 staphylococ
Q99u53 staphylococ
Q97te6 clostridium
                                                                                                                 Q48674 lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CMSITKKDANPNNGQTQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN
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NCBI_TaxID=2096;
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Pred. No. 2.2e-51;
3; Mismatches 4;
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Q49468 Q9KH15 Q9KH15 Q9L8D5 Q49500

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01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                NCBI_TaxID=2096;
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                                                                                           PMGA1.4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ENNVALQYTLNSGSAQEVNFAPTVKTSVSADSSGDSNNQTESAAETMPVTSDLNPAPTVS 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 GDEPSSRILA----NTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKLVKAAD
                                                                    Pherr G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D., May J.D., Hughlett M.B.;
"A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 EIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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43.4%; Pred. No. 2.5e-33;
.lve 75; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF210770; AF229524 1;
SEQUENCE 671 AA; 71898 MW; 4D6AE6B59175D679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                    671 AA
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O9L8D6;
01-0CT-2000 (TrEMBLrel. 15, Cr
01-0CT-2000 (TrEMBLrel. 15, La
01-0CT-2000 (TrEMBLrel. 15, La
PMGA-LIKE PROTEIN 9.2.
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Best Local Similarity 43.4%
Matches 179; Conservative
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|PSSRI 271
                                                                                                                                                                242 PSSRI 246
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STRAIN=S6;
MEDLINE=95010739; PubMed=7925999;
Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D.,
Markham P.F., Whithear K.G., Walker I.D.;
"The organisation of the multigene family which encodes the major cell
surface protein, pMGA, of Mycoplasma gallisepticum.";
FEBS Lett. 352:347-352(1994).
EBBS: L28424; AAA62418.1; -.
Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 TAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 WNGD-----EPSSRILANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                         Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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75517 MW; B70AC874FE85055C CRC64;
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Last annotation update)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     41.5%; Score 831.5; DB 2;
42.0%; Pred. No. 4.8e-33;
tive 84; Mismatches 116;
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NCBI_TaxID=29560;
                                                                                                                   Mycoplasmataceae; Mycoplasma
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                                   PMGA1.4 PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                   702 AA;
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Matches 173; Conserv
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69 NPNSGNTTPEQQLAAARKTLTDLLGTENTNVALYADYAKIQSTLSTAYMTAKTASENTSA 128
                                                                                                                 67 ILEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLSSTAYN 126
                                                                                                                                                                          127 QIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLSTINEQKTNADALS 186
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                                                           11 NPNNGQT-----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNNLNA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 DANPINGQTQLEAARME-----LTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                           NSFIKKVIQNNEQSFVGTFTNAN--VQPSNYSFVAFSADVTP------VNYKYARRT
                                                                                                                                                                                                                                                                                        236 VWNGD---EPSSRILLANTNSITDVSWIYSLAGINTKYQFSFSNYGPSTGYLYFPYKLVKA
                                                                                                                                                                                                                                                                                                                                                                             365 ADSSSVALQYSLNKTSSKLINFEPAKTMPTNADQSENGVATTSTTEGRSSSEVLVADEVA
                                                                                                                                                                                                                                                                                                                                                                                                          320 ANNTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAINHES;
Shen Q.C., Bi D.R., Weng C.J.;
"Sequence analysis of the pMGA multigene family of Mycoplasma sequence analysis of the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91414.1;
SEQUENCE 680 AA; 72909 MW; A2ABC6500E3DFE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
  Length 584;
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  40.2%; Score 805; DB 2; Length 58
42.4%; Pred. No. 7.6e-32;
tive 72; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                  ADANNVGLQYKLNNGNVQQVEF------ATST-----
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Query Match
Best Local Similarity 42.44
Matches 180; Conservative
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Best Local Similarity 39.89
Matches 164; Conservative
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SQGKI 484
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                                                                                                                                                                                                                                                              MEDLINE-99392472; PubMed-10463176;
Markham P.F., Duffy M.F., Glew M.D., Browning G.F.;
"A gene family in Mycoplasma imitans closely related to the pMGA family of Mycoplasma gallisepticum.";
Microbiology 145:2095-2103(1999).
EMBL; AF141940; AAD39483.1;
                                                                                                                                                                                                                    36;
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Shen O.C., Bi D.R., Weng C.J.;
Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.";
Submitted (JUN-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91415.1; -.
InterPro; IPR001986; EPSP_Syntase.
PROSITE: PS00104; EPSP_Syntase.
PROSITE: PS01004; EPSP_SYNTHASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma gallisepticum.
Bacteria; Firm.cutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID-2096;
                                                                                                                                                                                     ; Score 826; DB 2; Length 632;
; Pred. No. 8e-33;
65; Mismatches 120; Indels
                                                                                                                                     LHAL.
173F5B12E705BE47 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                 POTENTIAL.
                                                                                                                                           66959 MW;
                                                                                                                                                                                      41.28;
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Best Local Similarity 45.3%
Matches 183; Conservative
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632 AA;
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                                                                                                       -----ATSTSANNTTANPTPAV 331
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                                                                                                                                                                                                                                                                        TVWNGD-----EPSSRILANTNSITDVSWIYSLAGTNTKYQFSFSNYGPSTGYLYFPYKL
                                      QEKYSAILSEINAASSTAEEIVKQTLNPVNG-----NLPVVAALNAENTKILEAIKEEK
                                                                                  INEQKTNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPVNYKYARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S6; Markham-S510739; PubMed-7925999; Bowden T.R., Pollocks T.D., Markham P.E., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; Which encodes the major "The organisation of the multigene family which encodes the major surface protain, pMGA, of Mycoplasma gallisepticum."; FEBS Lett. 352:347-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID-2096;
                                                                                                                                                                                                                                                                                                                              332 DEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADK 383
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75537 MW; 273E8915FEE57B9F CRC64;
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Last annotation update)
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41.6%; Pred. No. 2.8e-29;
cive 62; Mismatches 127;
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01-DEC-2001
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                                                                                  NTTANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENNA 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AAQYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTADVVMMANTKIVEAIKDEVLNPQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
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                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=PG31, ATCC19610;
MEDLINE=99003182; PubMed=9784576;
MLLIU L., Payne D.M., van Santen V.L., Dybvig K., Panangala V.S.
A protein (M9) associated with monoclonal antibody-mediated agglutination of Mycoplasma gallisepticium is a member of the I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.2%; Score 746; DB 2; Length 64:
42.3%; Pred. No. 6.2e-29;
iive 64; Mismatches 123; Indels
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EMBL, AF032890, AAC69269.1, -.
SEQUENCE 645 AA; 69876 MW; 5A2F29572CFAE055 CRC64;
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Last annotation update)
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NCBI_TaxID=2096;
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Matches 172; Conservative
ANNVGLQYKLNNGNVQQVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum.
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQKTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 QYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTAGAVTMANTKIVEAIKDEVLNPKKEN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSANNTTAN-PTPAVDEIKVAKIVLSG 343
                                                                                                                                                                                                                                                                                                                          Gaps
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                            Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; Prie organisation of the multigene family which encodes the major surface protein, PMGA, of Mycoplasma gallisepticum."; FEBS Lett. 352:347-352(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 ADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKYAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Markham P.F., Glew M.D., Sykes J.E., Bowden T.R., Pollocks T.D., Browning G.F., Whithear K.G., Walker I.D.; "The organisation of the multigene family which encodes the major surface protein, pwGA, of Mycoplasma gallisepticum.";
                                                                                                                                                                                                                                                                                                                                                       NPNNGQ------TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVNNN
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NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                            Length 650;
                                                                                                                                                                                                                                                                                         37.1%; Score 744; DB 2; Length 65
42.9%; Pred. No. 7.9e-29;
ive 62; Mismatches 127; Indels
                                                                                                                                                Markham P.F.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90714; AAB50152.1; -.
                                                                                                                                                                                                                                 HAEMAGGLUTININ.
3ABACDB65940EBBB CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 LRFGONTIELSVPTGEGNMNKVAPMIGNIYLSSNENNADKI 384
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STRAIN=56;
MEDLINE=95010739; Pubmed=7925999;
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650 HA
70249 MW;
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Best Local Similarity 42.99
Matches 172; Conservative
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26 6
650 AA;
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01-DEC-2001
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049497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 DINPGDGGGMMNAASQELAAARMGLTTVFDSKAKNLGLYVDYKKTQDTLTKAYDAAKTVL 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                           STRAIN-PG31, ATCC19610;
MEDLINE-99003182; PubMed-9784576;
Liu L., Payne D. M., van Santen V.L., Dybvig K., Panangala V.S.;
"A protein (M9) associated with monoclonal antibody-mediated agglutination of Mycoplasma gallisepticum is a member of the pMGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNADALSNSF1KKV1QNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY
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                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                 37.2%; Score 745; DB 2; Length 644;
42.3%; Pred. No. 7e-29;
ive 65; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                      644 AA; 69866 MW; 8B9F352B13FBDE5C CRC64;
                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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Last annotation update)
               644 AA
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               PRT;
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EMBL, AF053978; AAC69274.1; -.
Hypothetical protein.
                                                                                         HYPOTHETICAL 69.9 KDA PROTEIN.
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049495; 008060;
01-NOV-1996 (TYEMBLYEL). 01, C3
01-NOV-1998 (TYEMBLYEL). 01, L6
01-NOV-1998 (TYEMBLYEL). 08, L6
HAEMAGGLUTININ PRECURSOR.
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NCBI_TaxID=2096;
                                                                                                        Mycoplasma gallisepticum.
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Best Local Similarity 42.39
Matches 172; Conservative
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                                                                                                                                                  NCBI_TaxID=2096;
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                              Q9ZHR9
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Best Local Similarity 41.0
Matches 166; Conservative
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SEQUENCE FROM N.A.
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ID Q9KH15
AC Q9KH15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TNADALSNSFIKKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----NYKY 231
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                                                                                                                                                                                                                                                              108 DNSSSTTQNLNEAKTRLETAIRTAATSKQTFDEQHAELVKVYKELKTTLSNETATLAPYA 167
                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                      9 DANPINGO-----TQLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE-93162830; PubMed-8432610;
MATKham P.E., Glew M.D., Whithear K.G., Walker I.D.;
"Molecular cloning of a member of the gene family that encodes hemaglutinin of Mycoplasma gallisepticum.";
Infect. Immun. 61:903-909(1993).
EMBL; M83178; AAA02996.1;
                                                                                                                                                                                          48;
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                                                                                                                                                                                          Indels
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647 HEMAGGLUTININ HOMOLOG.
70333 MW; 33916673BB9E28C4 CRC64;
                                                                 POTENTIAL.
356554BD2C72C1F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TremBLrel. 01, Created)
1-NOV-1996 (TremBLrel. 01, Last sequence update)
01-NAY-2000 (TremBLrel. 13, Last annotation update)
HEMAGCITININ HOWOLOG PRECURSOR.
                                                                                                                                                37.1%; Score 743; DB 2;
42.3%; Pred. No. 8.8e-29;
tive 62; Mismatches 125;
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                                                                 25 PC
70205 MW;
FEBS Lett. 352:347-352(1994).
EMBL: L28424; AAA62416.1; -.
SIGNAL.
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SIGNAL.
SEQUENCE 649 AA; 70205 MW;
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NCBI_TaxID=2096;
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647 P
                                                                                                                                                Query Match
Best Local Similarity
Matches 172; Conserv
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Best Local Simi
Matches 169;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                    NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
                                                                                                   DAQYAGIKMHLSGLYDAGKAITTKTLEPVEGDP-LTASAVMMANTKIVEAIKDEVLNPQK 226
                                                                                                                                                                                                                                                                                                                                                                                                     STGYLYFPYKLVKAADANNVGLQYKLNNGNVQQVEFATSTSA-----NNTTANPTPAVDE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 DANPINGQT-----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 TNADALSN--SFI--KKVIQNNEQSFVGTFTNANVQPSNYSFVAFSADVTPV-----
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                                                                                                                                                                           STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTL--STINEQK
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                                                                                                                                                                                                                                                                                                                                                                         NYKYARRTVW-NGDEPSSRILLANT-----NSITDVSWIYSLAGTNTKYQFSFSNYGP
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"Sequence analysis of the pMGA multigene family of Mycoplasma gallisepticum strain HS.';
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275312; AAF91413.1; -
SEQUENCE 656 AA; 70875 MW; 58EA7E075FC617E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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Last annotation update)
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Search completed: June 12, 2002, 10:50:42 Job time: 205 sec
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VRETGLAFGKNT 419
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TGYLYFPYKLVKAADANNVGLQYKLN-NGNVQQVEFATSTSANNTTANPTPAVDEIKVAK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 PQGVEPAQQQGDSSPKQASETQEVSPTPAAEVQAQQADTEQPATSQGTPLTDVSWIYSLS 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CMSITKKDANP-----QLEAARMELTDLINAK 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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EMBL: 090714; AAB50154.1; -
InterPro: IRR002819; HD
SEQUENCE 703 AA; 75742 MW; 310B69BE9F73CBC5 CRC64;
                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                     703 AA.
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01-DEC-2001 (TrEMBLrel.
HAEMAGGLUTININ.
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Best Local Similarity
Matches 167; Conserv
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STAYNQIRNNLVDLYNKASSLITKTLDPLNGGTLLDSNEITTANKNINNTLS--TINEQK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNLNATLEQLKMAKTNLESAINQANTDKTTFDNEHPNLVEAYKALKTTLEQRATNLEGLS 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DANPNNGQT-----QLEAARMELTDLINAKAMTLASLQDYAKIEASLSSAYSEAETVN 61
                              --GPAASVDNINVAKVNLANLNFGENTIEFSVP-----MNKVAPMIGNMYITSDVAN 485
324 TANPTPAVDEIKVAKIVLSGLRFGQNTIELSVPTGEGNMNKVAPMIGNIYLSSNENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharr G.T., Branton S.L., Hanson L.A., Minion F.C., Lott B.D., May J.D., Hughlett M.B.; "A novel pMGA-like gene from the F-strain (vaccine strain) of
                                                                                                                                                                                                                                                      01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2000 (TrEMBLrel. 15, Last annotation update)
PMGA-LIKE PROTEIN 9.3 (FRAGMENT).
Mycoplasma qallisepticum.
Macoplasma qallisepticum.
Mycoplasma qroup; Mollicutes; Macoplasma group; Mollicutes;
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210770; AF229525.1; -.
NON.TER 419 419
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